

Figure 1a

	MS-GPC- 8-27-7	MS-GPC- 8-27-10	MS-GPC- 8-6-13	MS-GPC- 8-27-41	MS-GPC- 8-6-47	MS-GPC- 8-10-57	MS-GPC- 8-6-27	MS-GPC- 8	MS-GPC- 8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone -BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme human	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

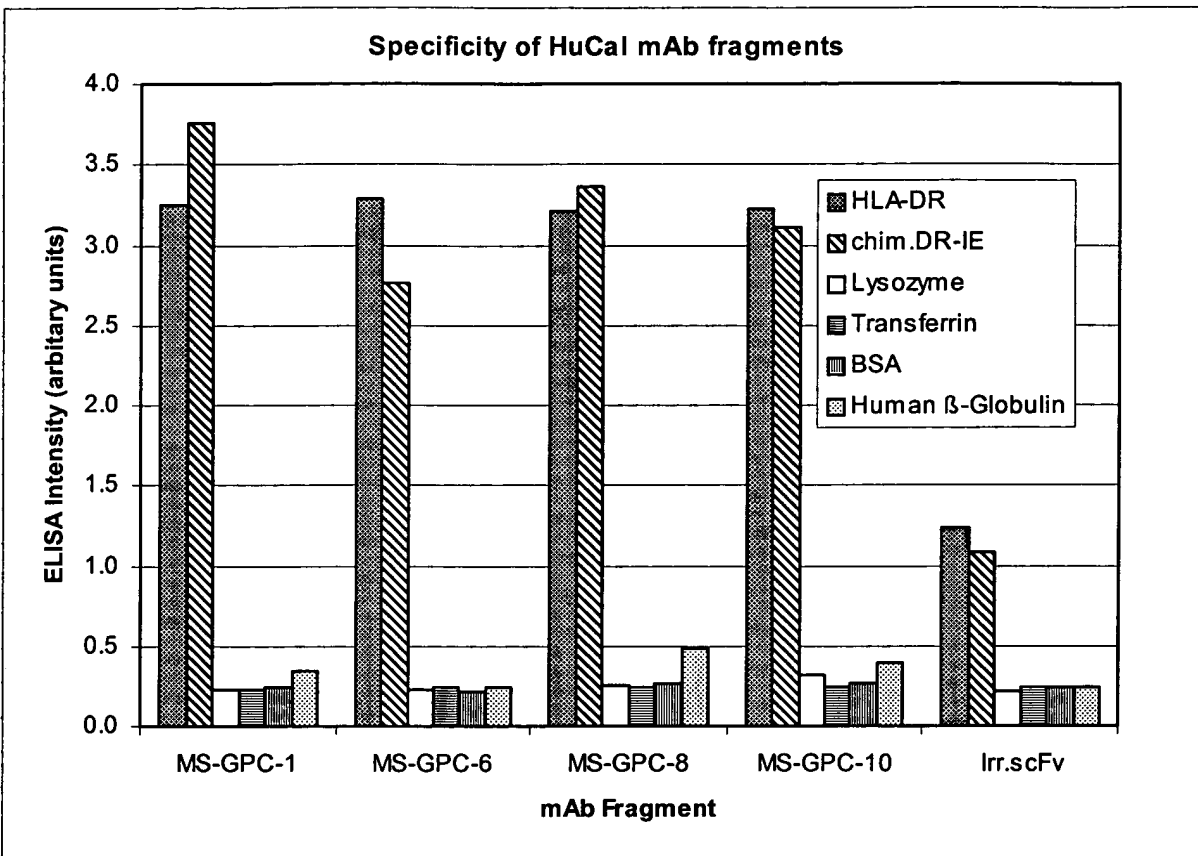
Figure 1c

Target Proteins	scFv											IgG			
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
DR4Dw4 Purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lysozyme	- <sub>b</sub>	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a. In Elisa, OD (at 370 nm - background): &gt; 1.5

b. In Elisa, OD (at 370 nm - background): &lt; 0.5

**Figure 1b**



**Figure 2**

Cell Line	HLA-	DRB1*	scFv											IgG			
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	ID09C3	1C7277	305D3
LG2	DR1	0101	+ <sup>a</sup>	+	- <sup>b</sup>	-	+	+	+	+	+	+	+	+	+	+	+
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+/- <sup>c</sup>
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+/-
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
L105.1	DRw52	B3*0101	+	-	-	-	nt <sup>d</sup>	+	-	+	+	+	nt	nt	+/-	+/-	+/-
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt
Target Cell			% Cells Killed <sup>e</sup>														
PRIESS			75	20	28	32	22	89	33	59	75	34	1	5	88	93	74

a. FACS analysis, mAb + FITC-anti human IgG<sub>4</sub>, mean fluorescence intensity > 30.

b. Mean fluorescence intensity < 10.

c. Mean fluorescence intensity 10-30.

d. Not tested.

e. Based on viable cell recovery after treatment with 200 nM scFv plus 100 nM anti-FLAG or 50 nM mAb at 37 °C for 4h. Determined by light.

Figure 3

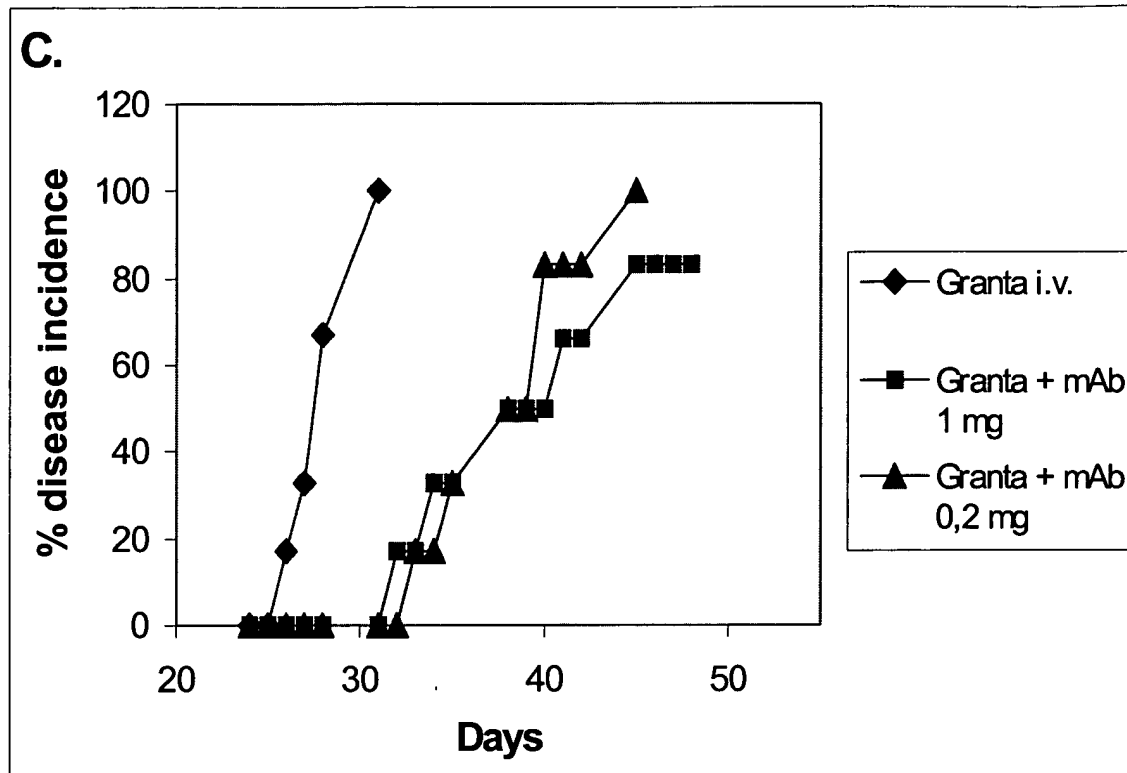
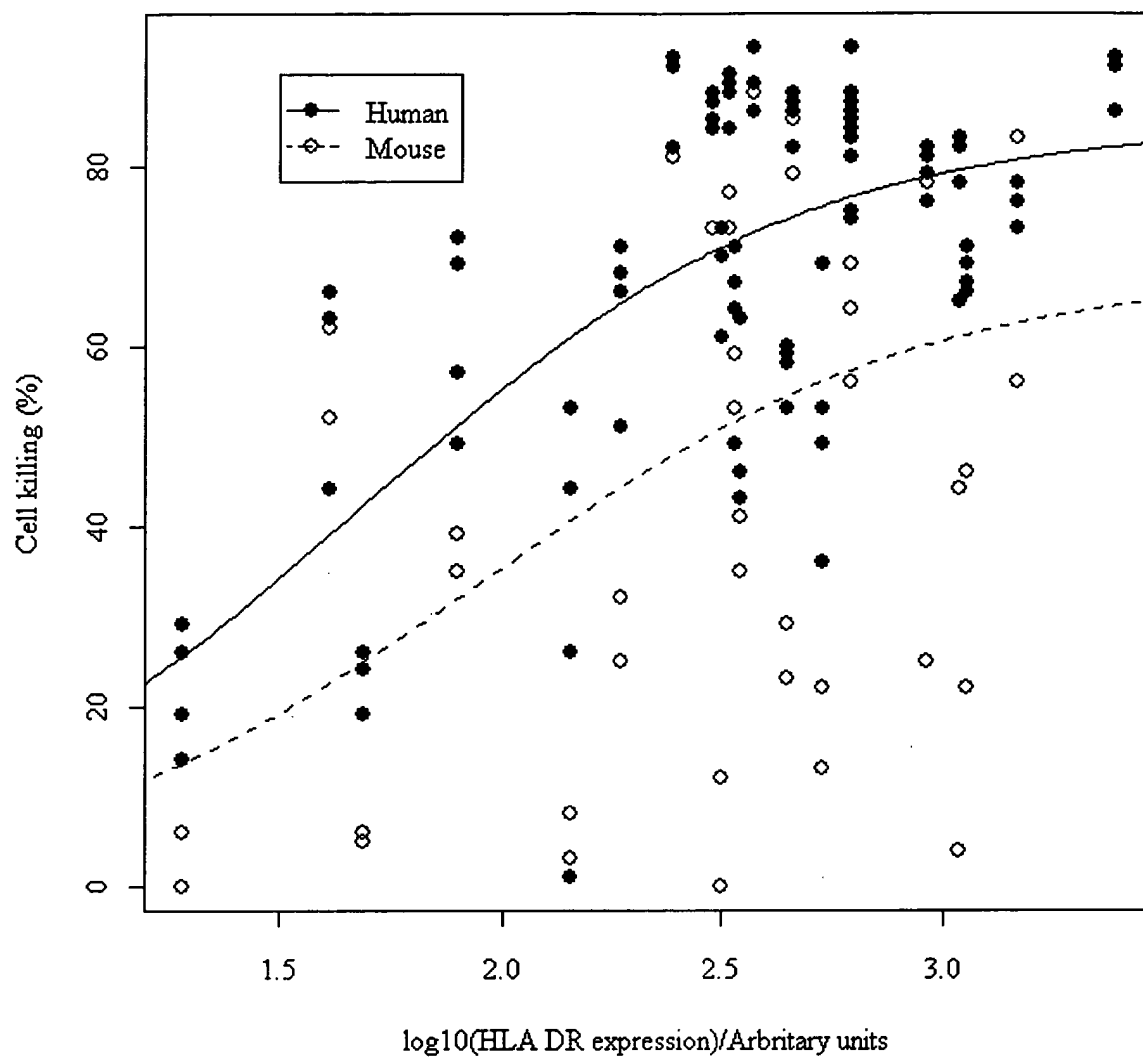


Figure 4



**Figure 5**

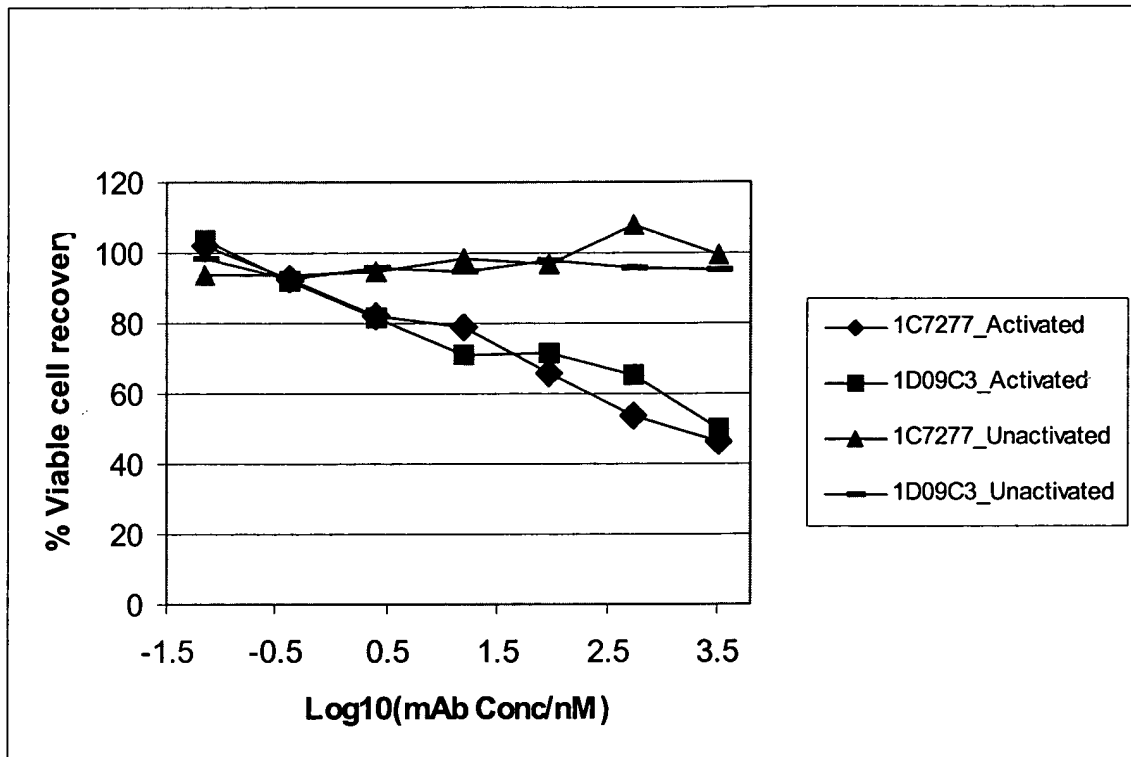
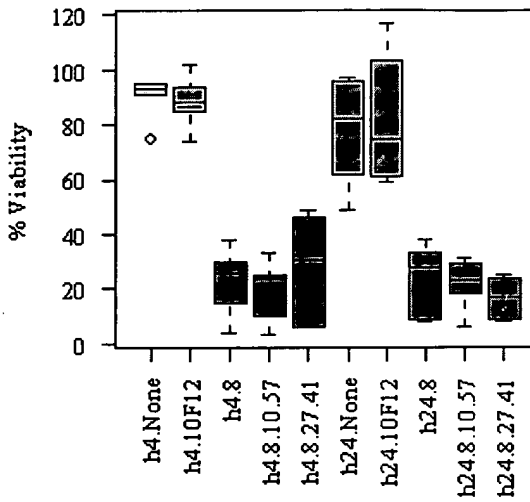
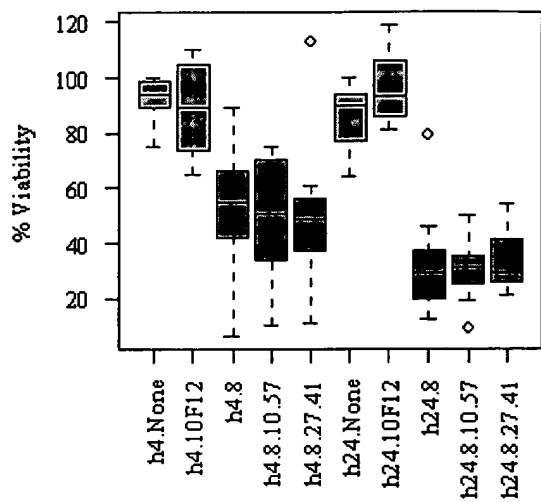


Figure 6a



**Figure 6b**

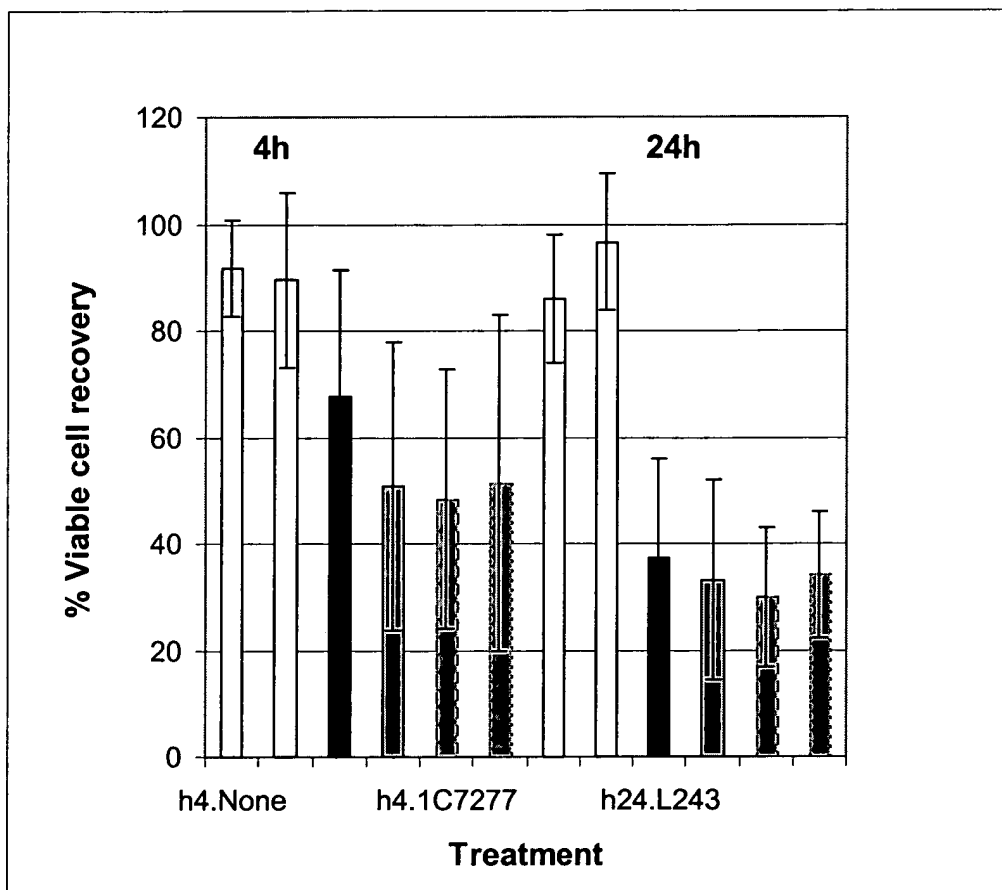




Figure 6c

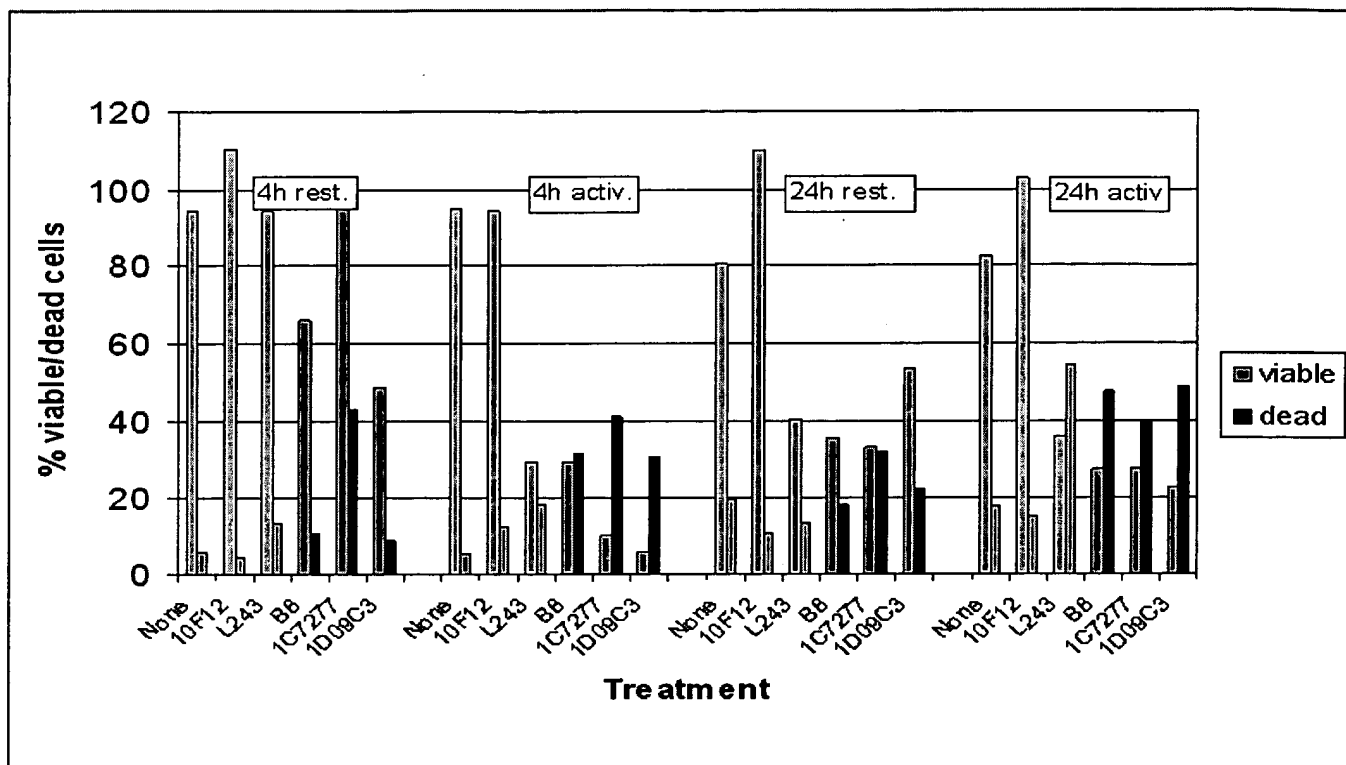
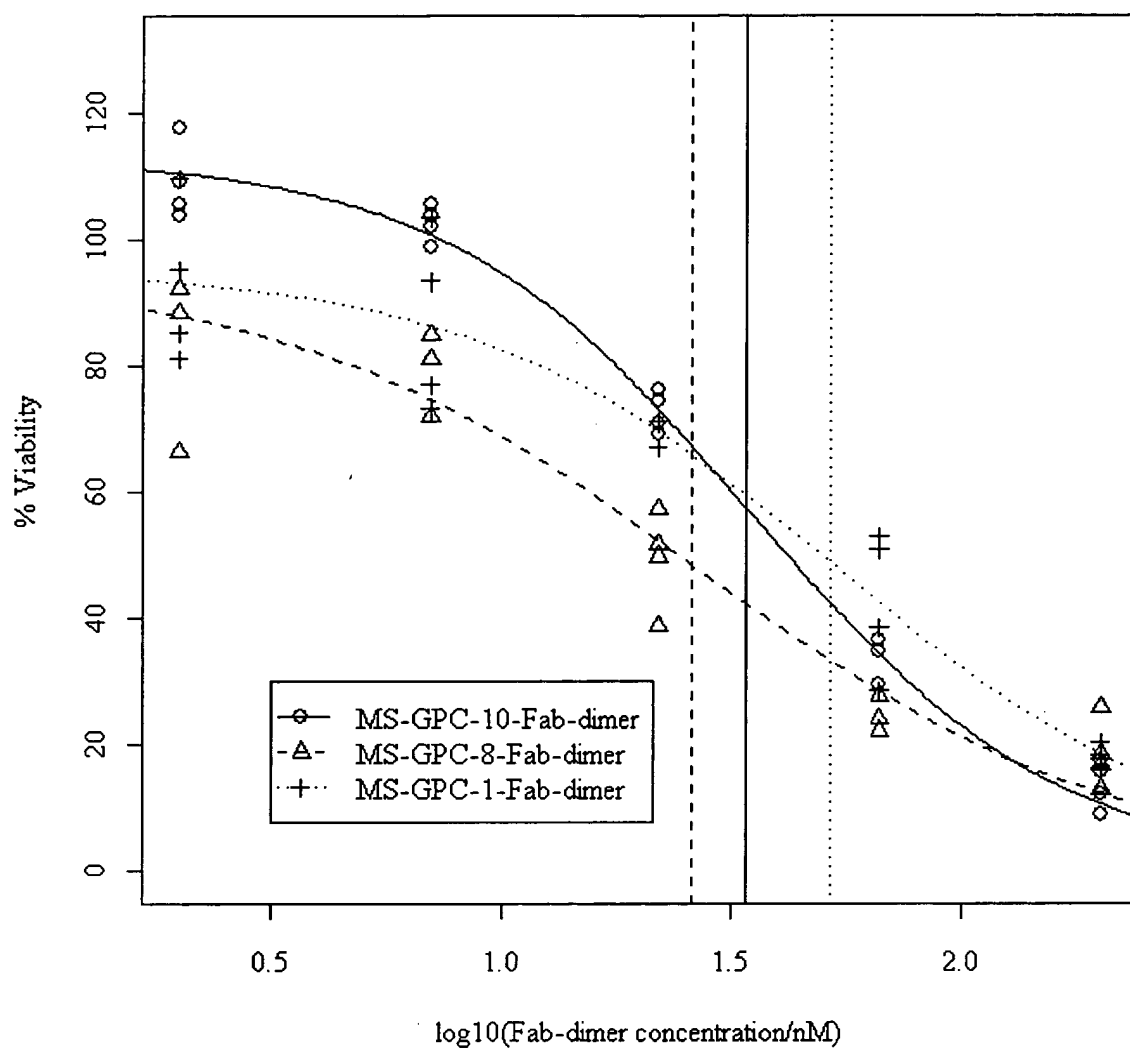


Figure 7a



**Figure 7b**

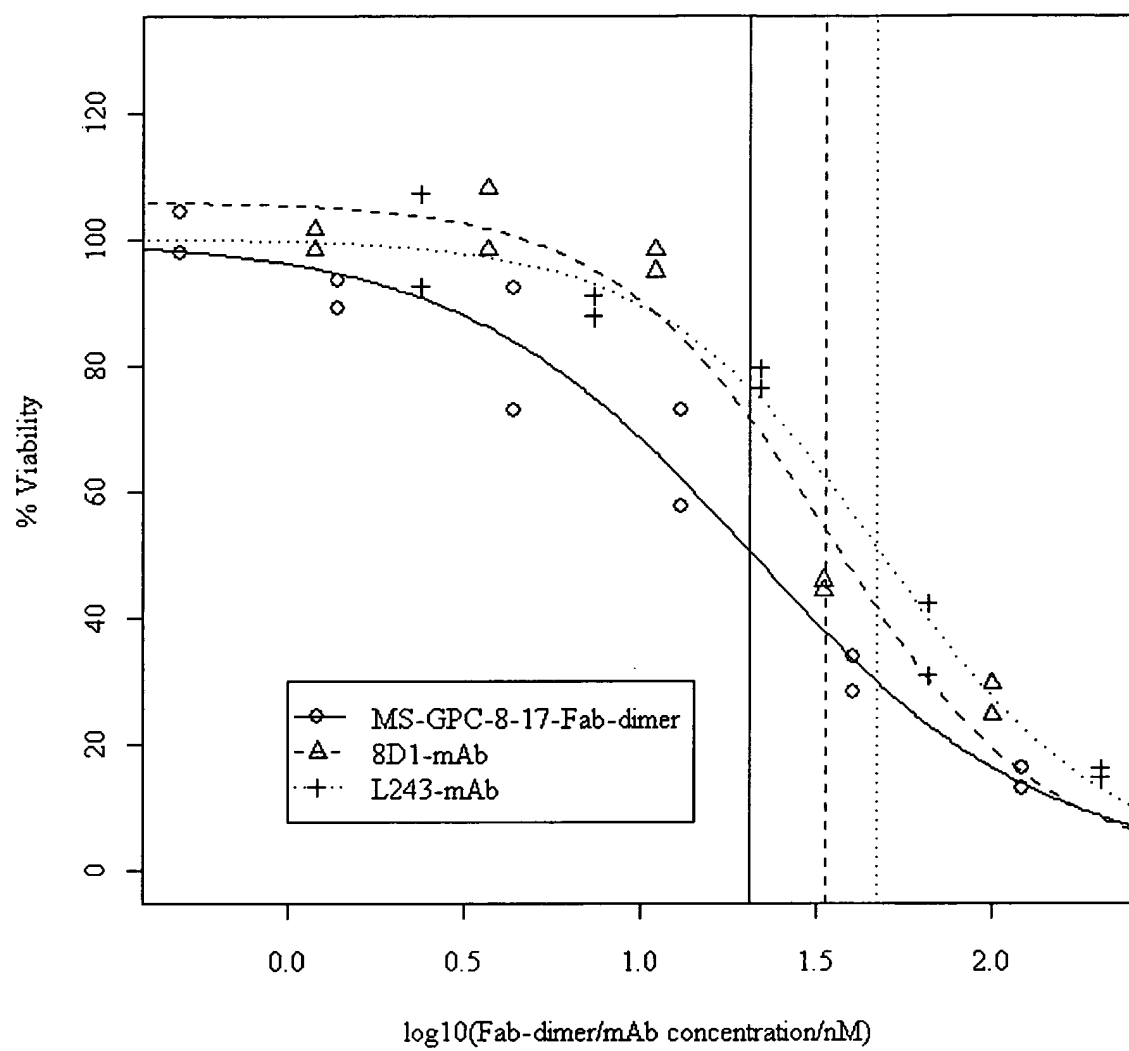


Figure 7c

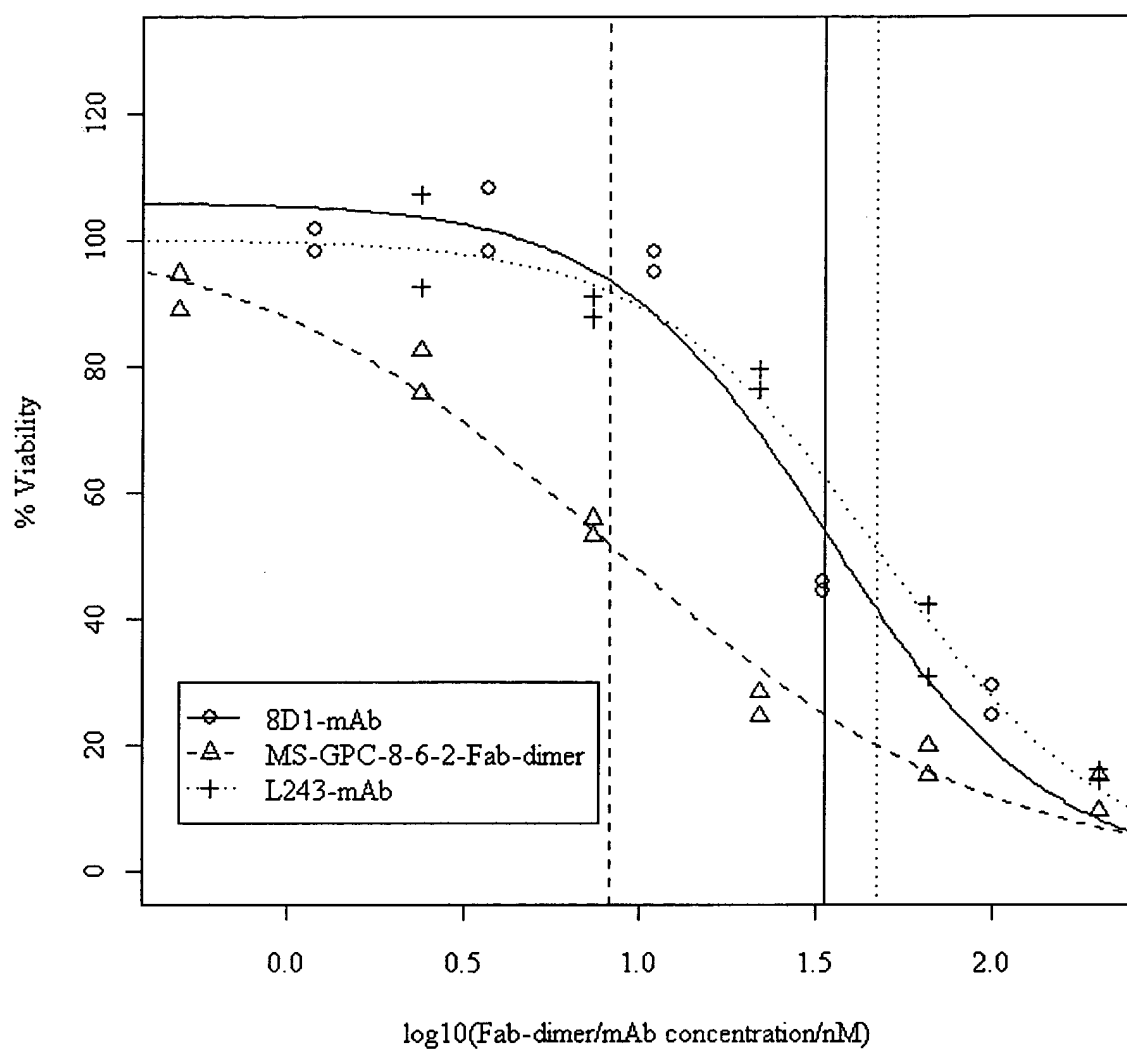
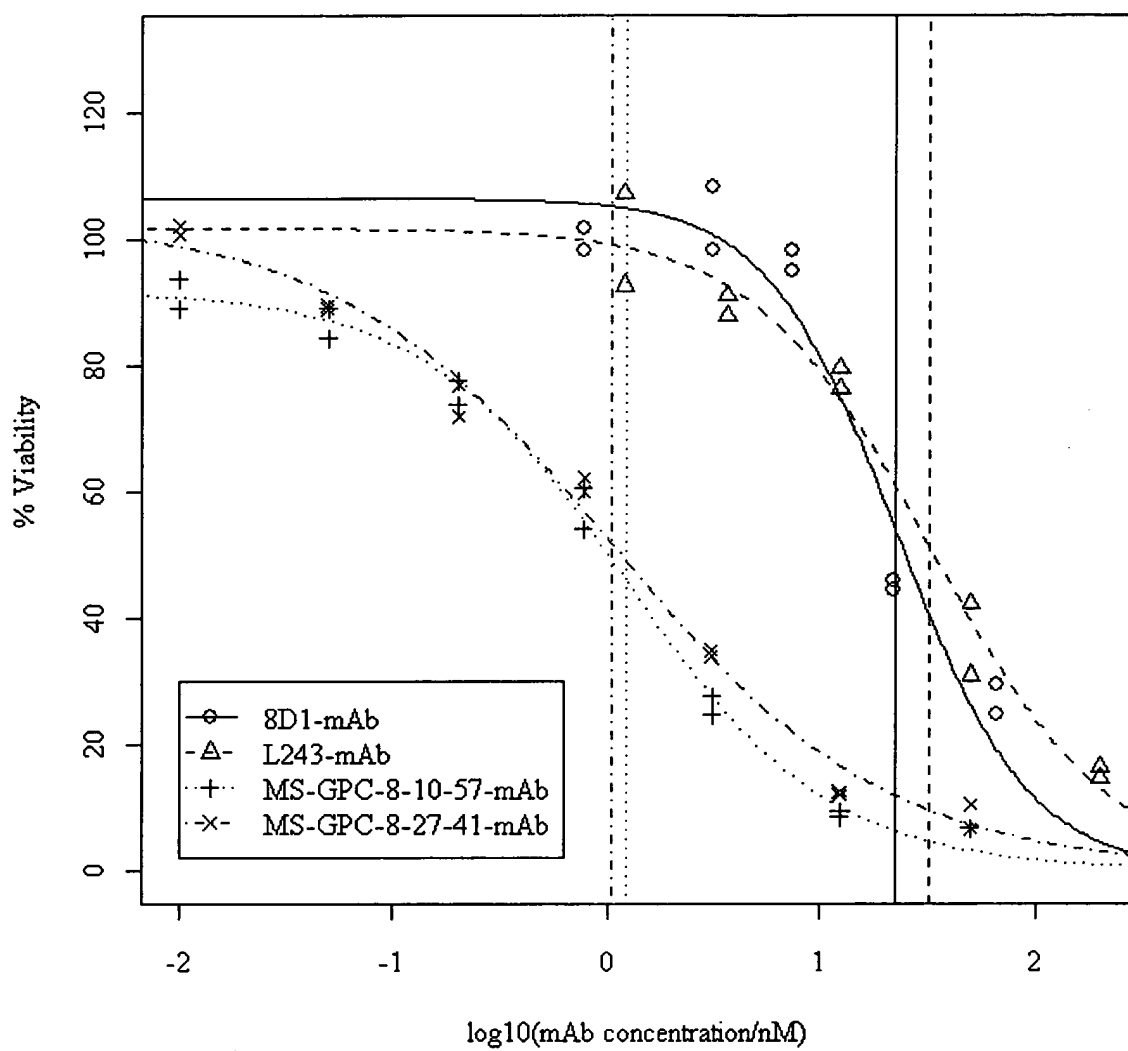


Figure 7d



**Figure 8a**

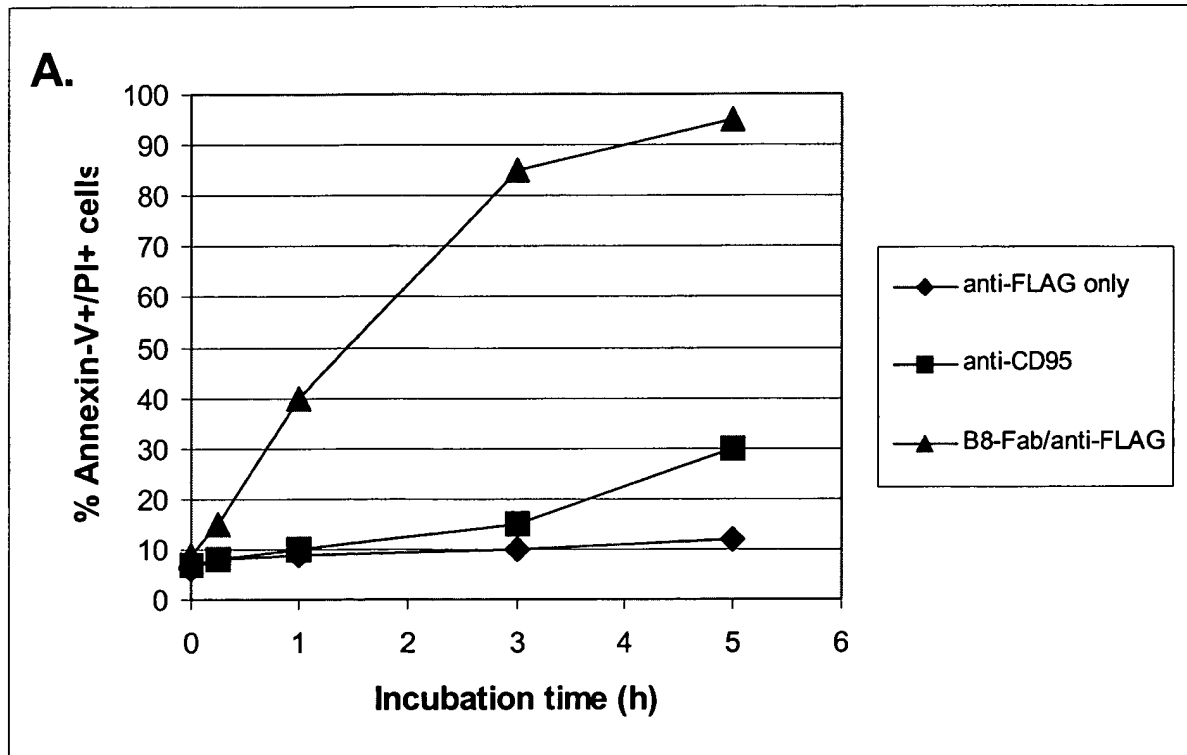


Figure 8b

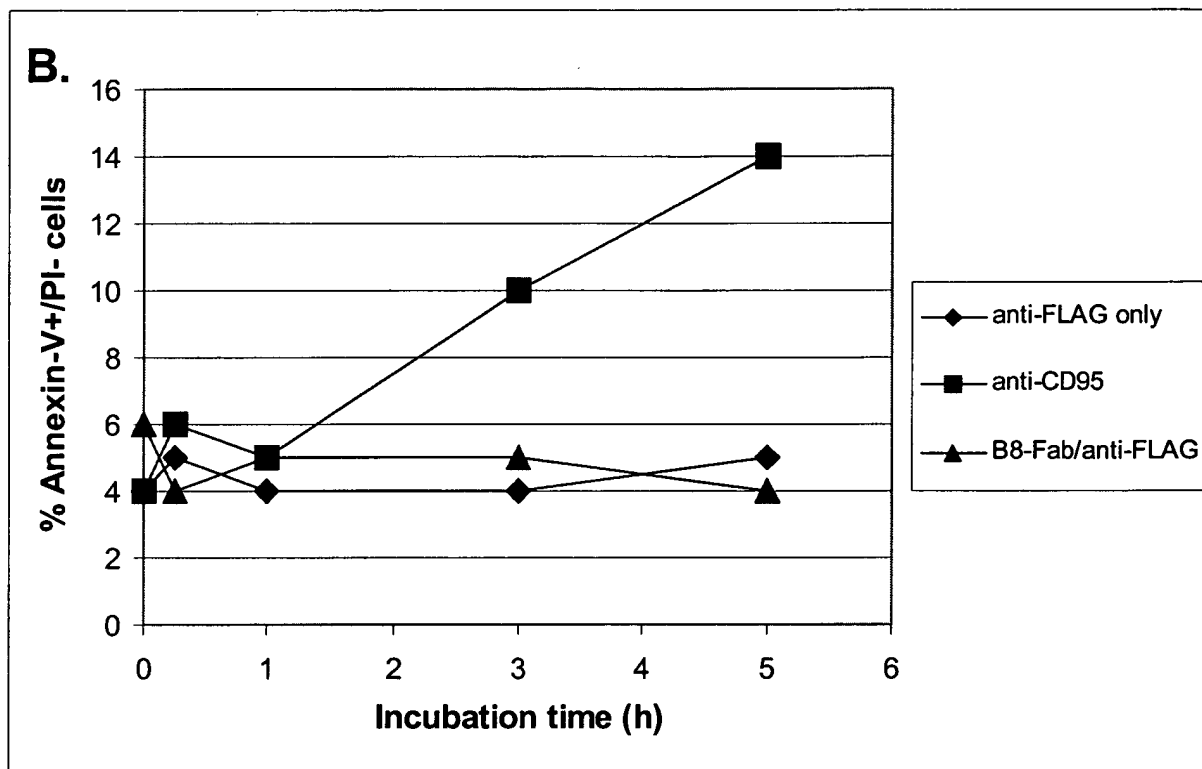


Figure 8c

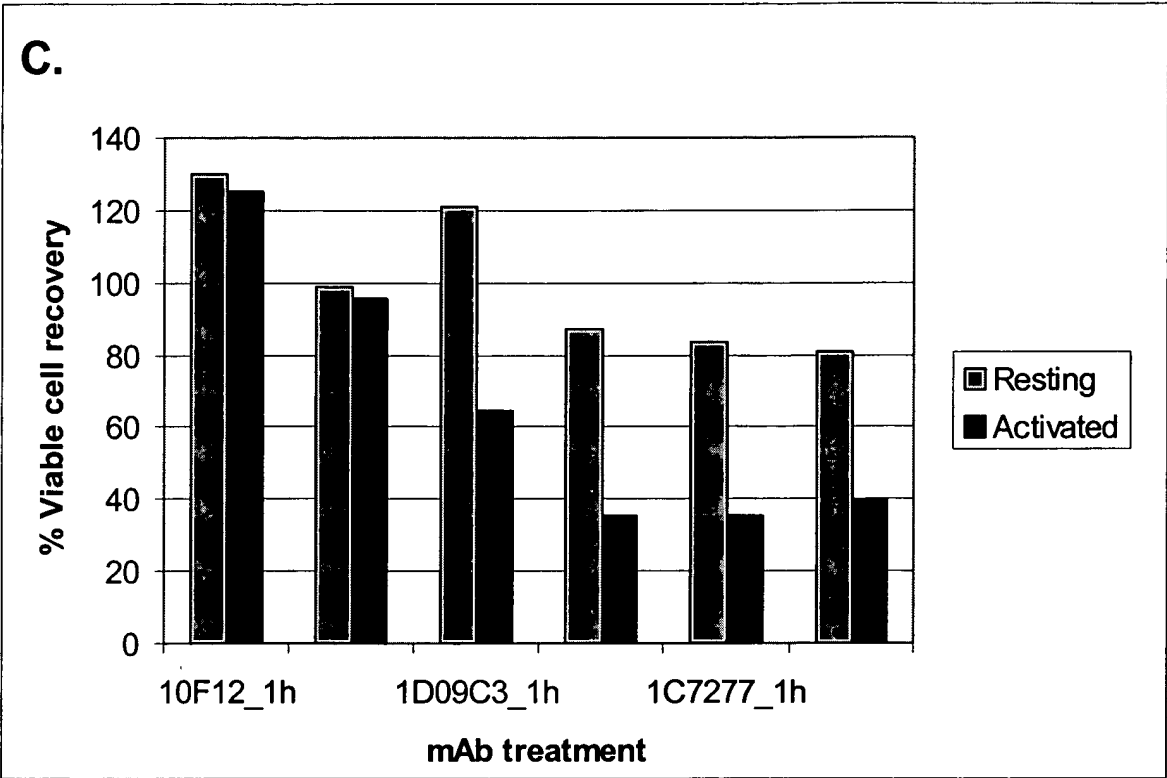




Figure 9a

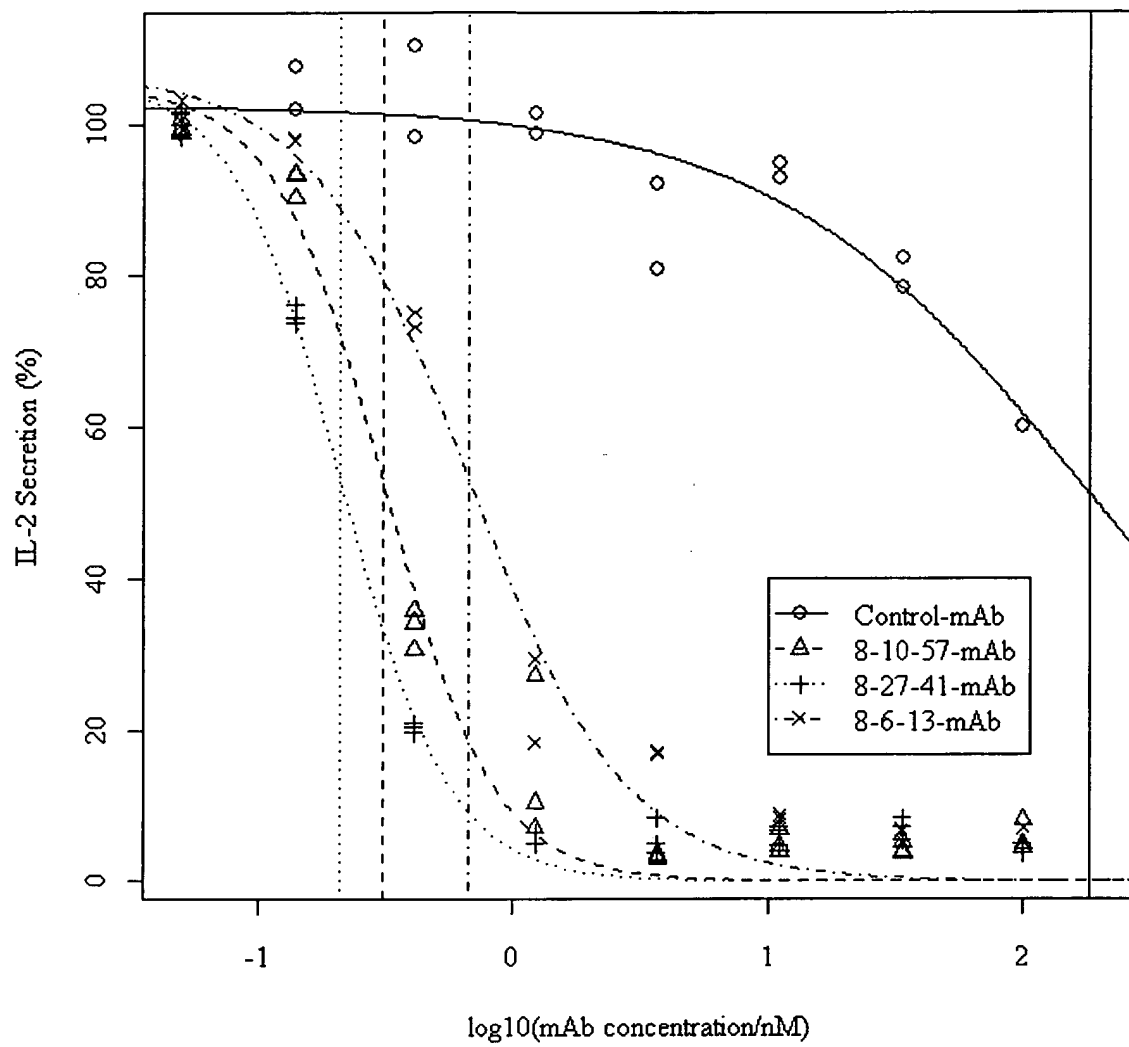


Figure 9b

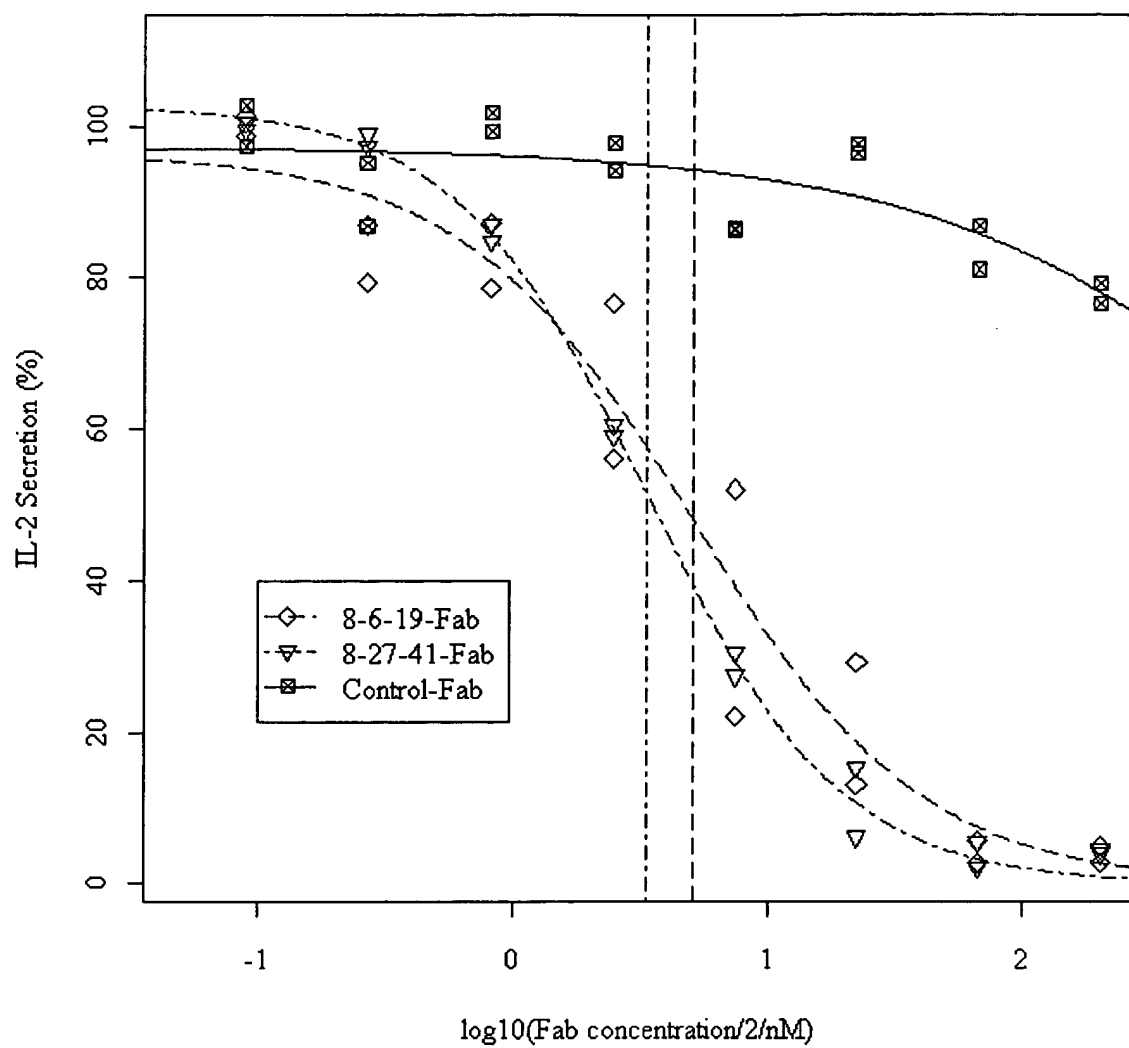


Figure 9c

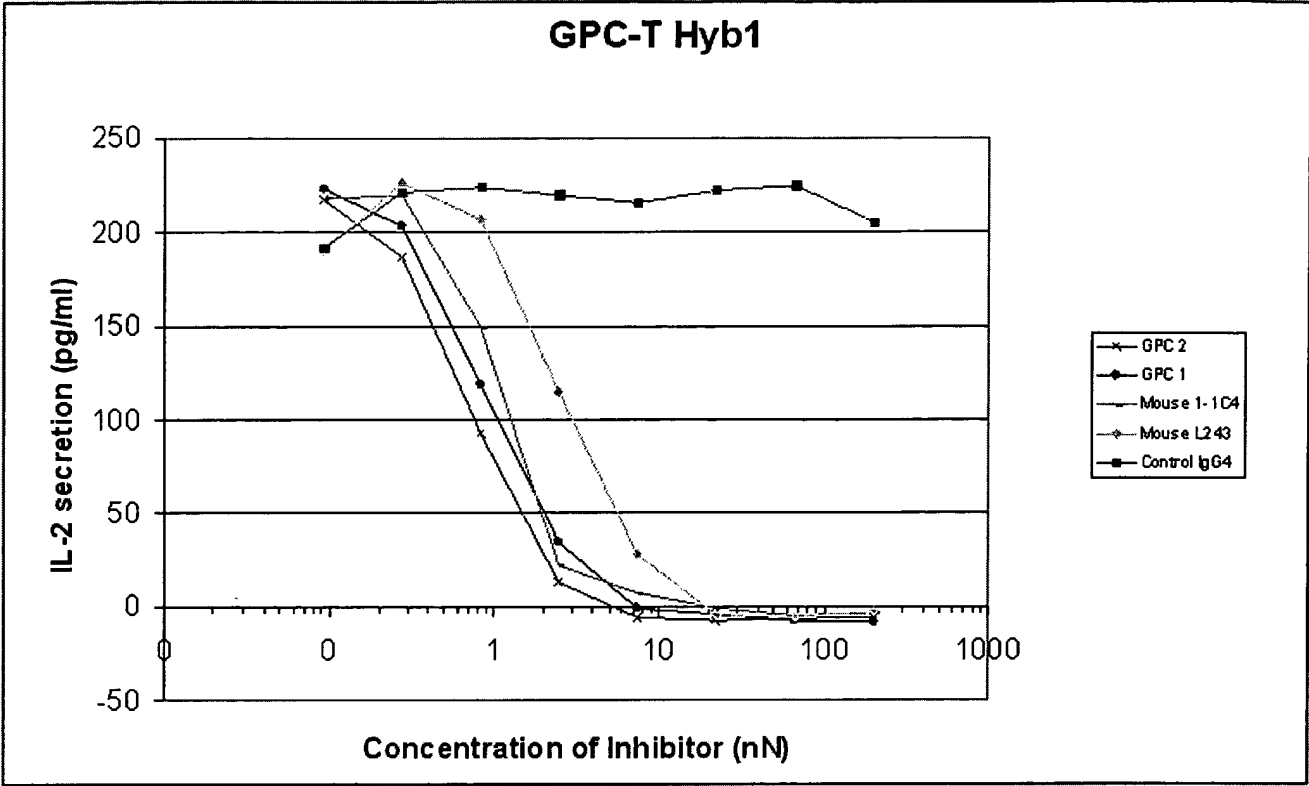


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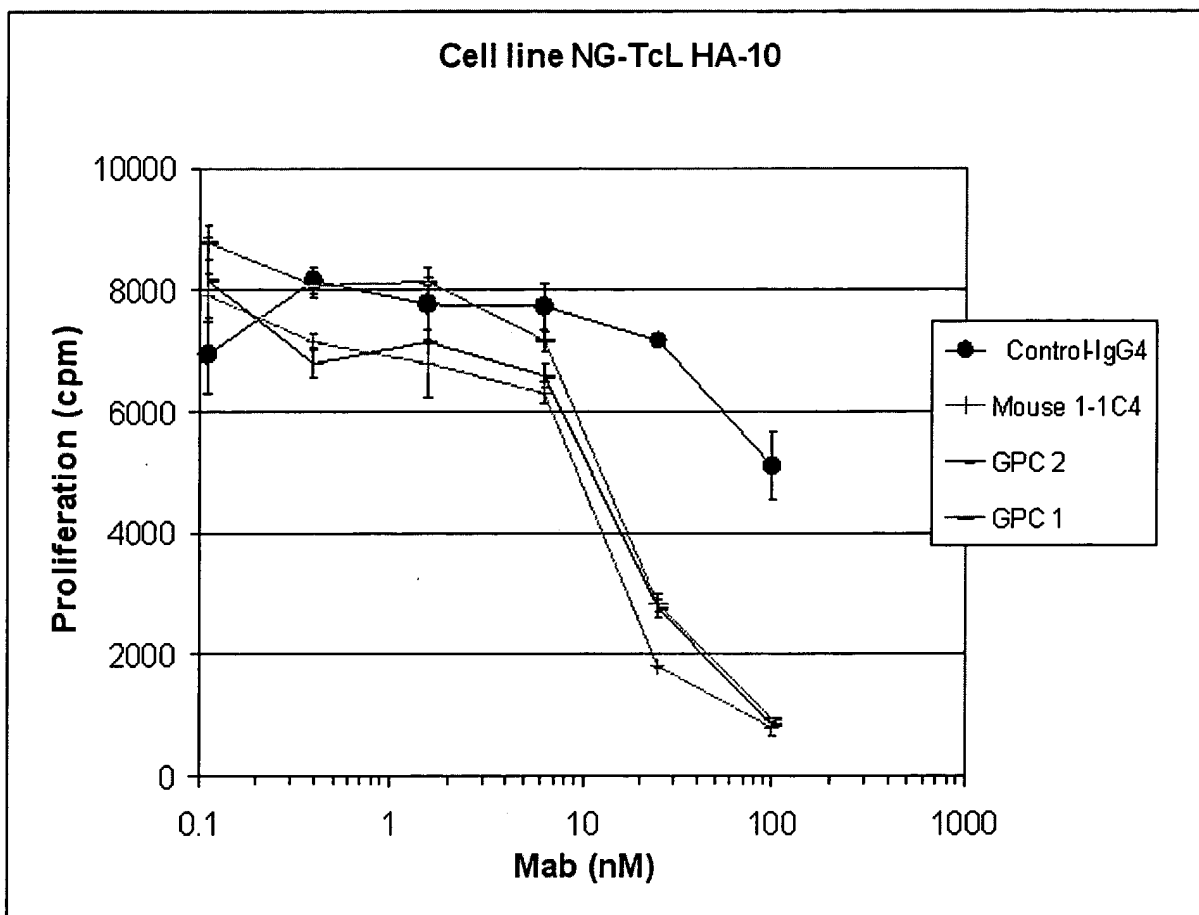


Figure 9e

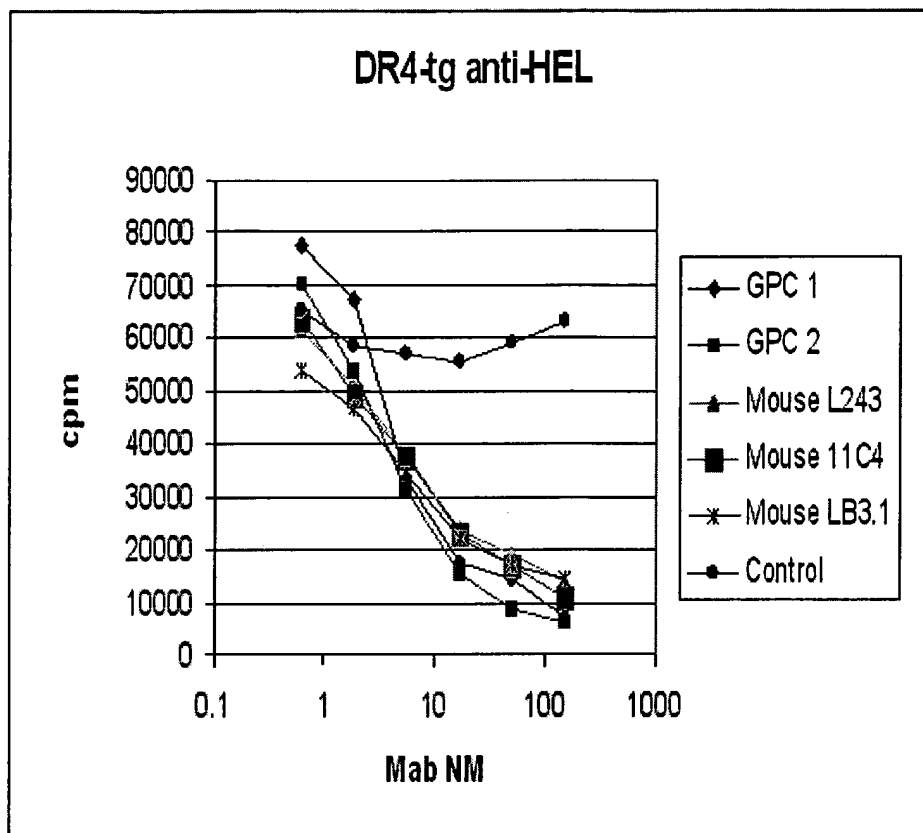


Figure 9f

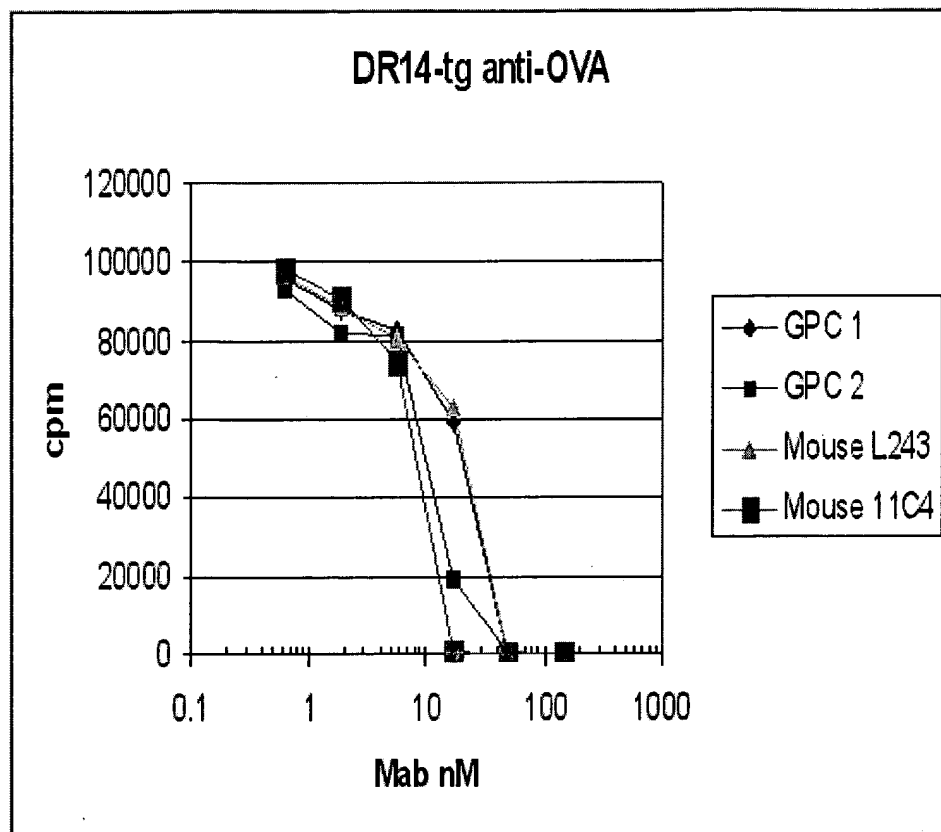
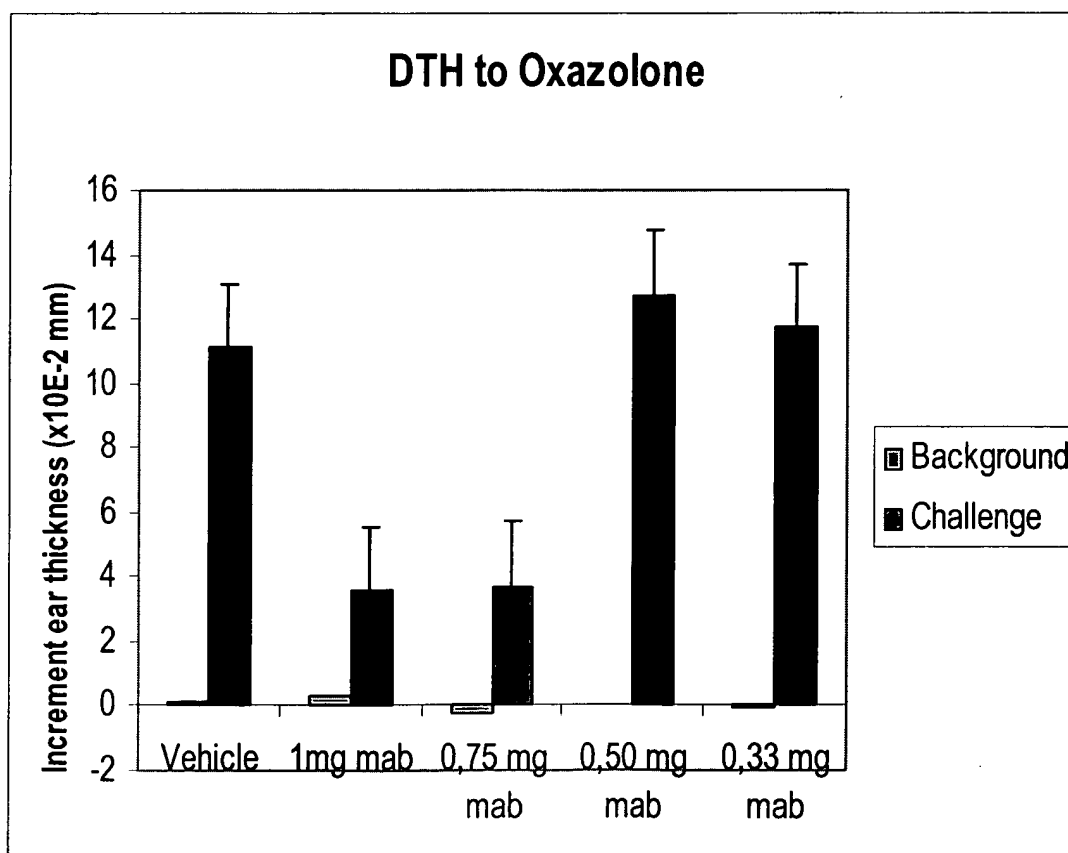
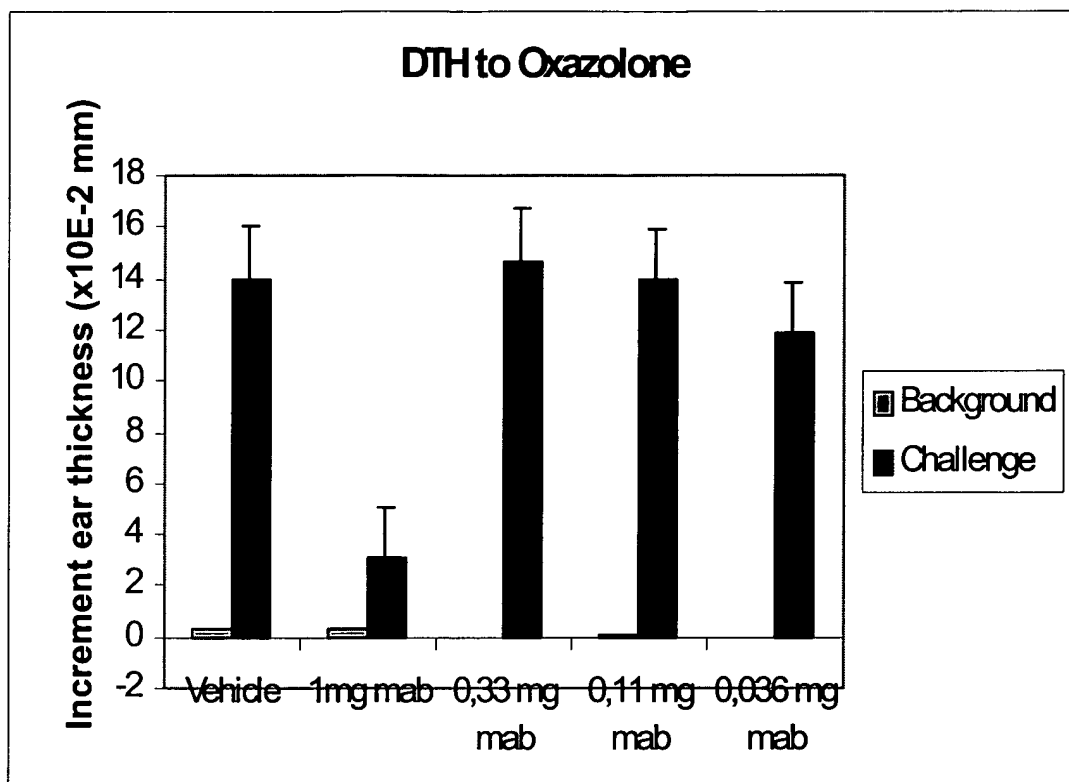
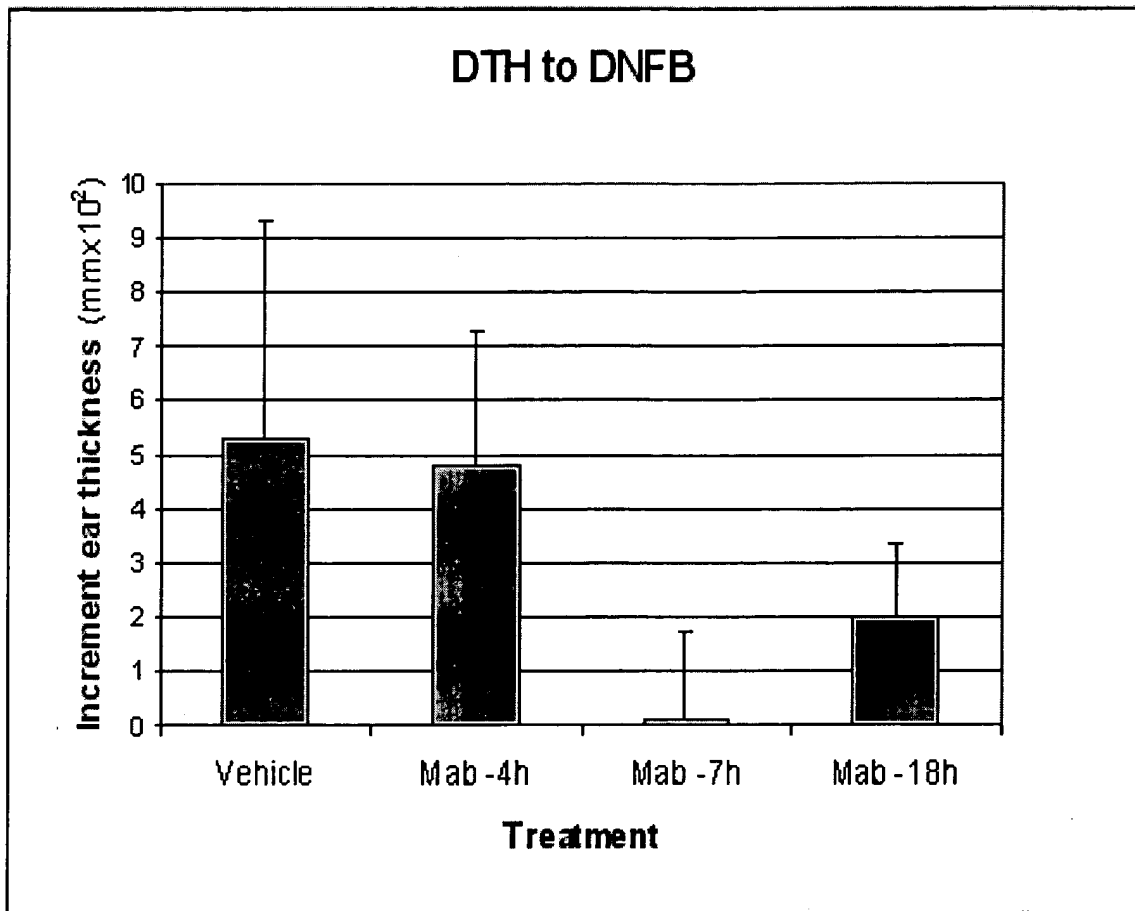


Figure 9g



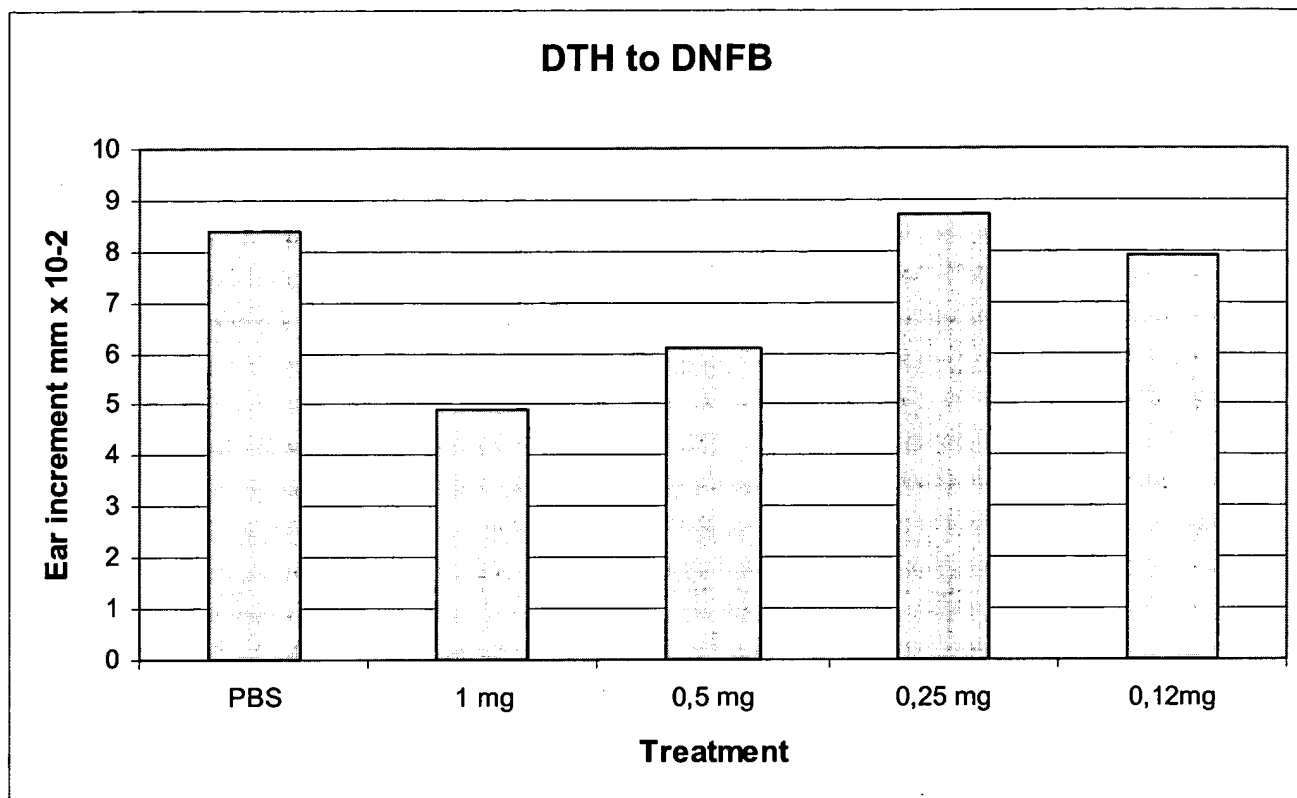
**Figure 9h**



**mAb: 1D09C3**

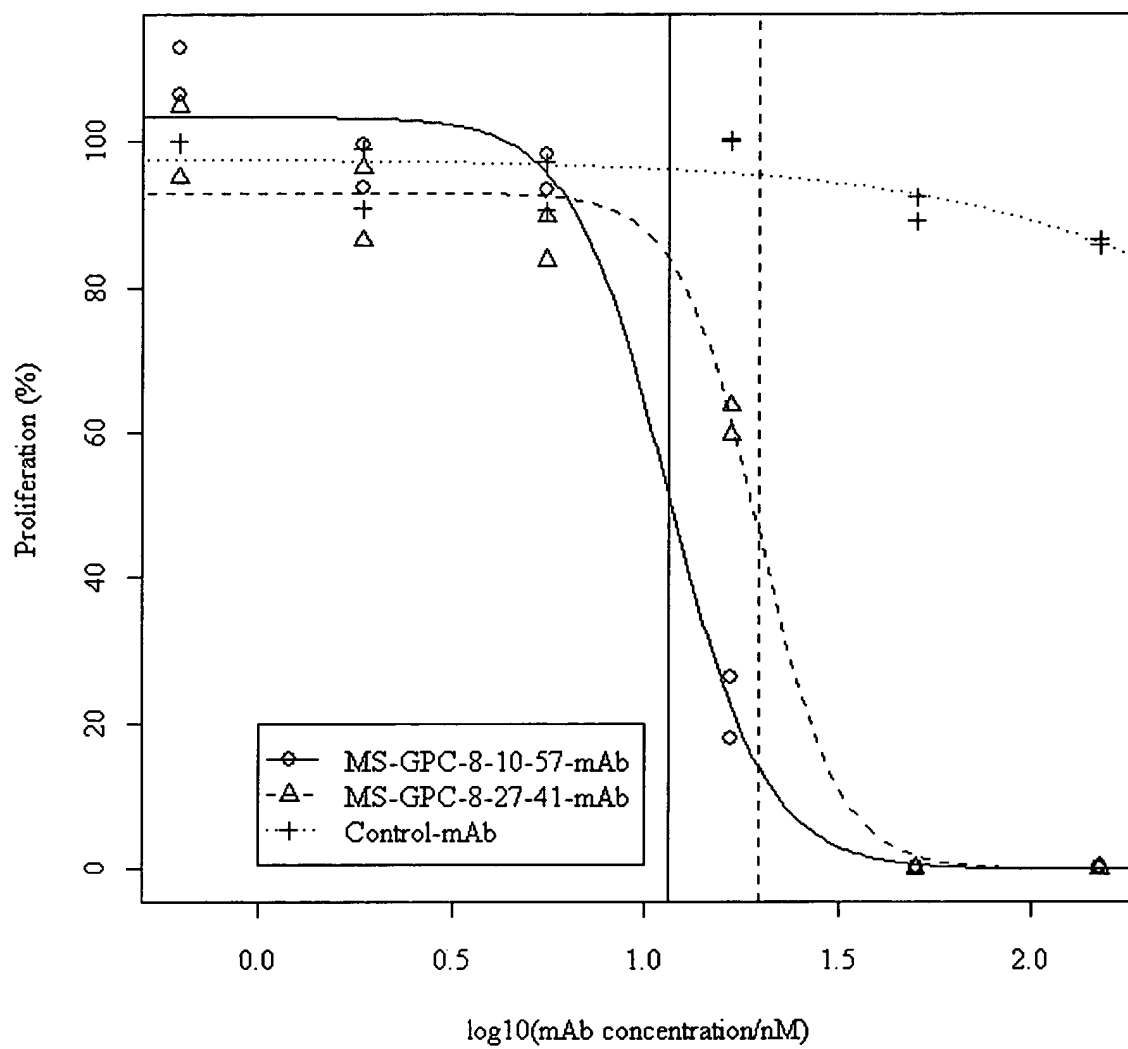


**Figure 9I**

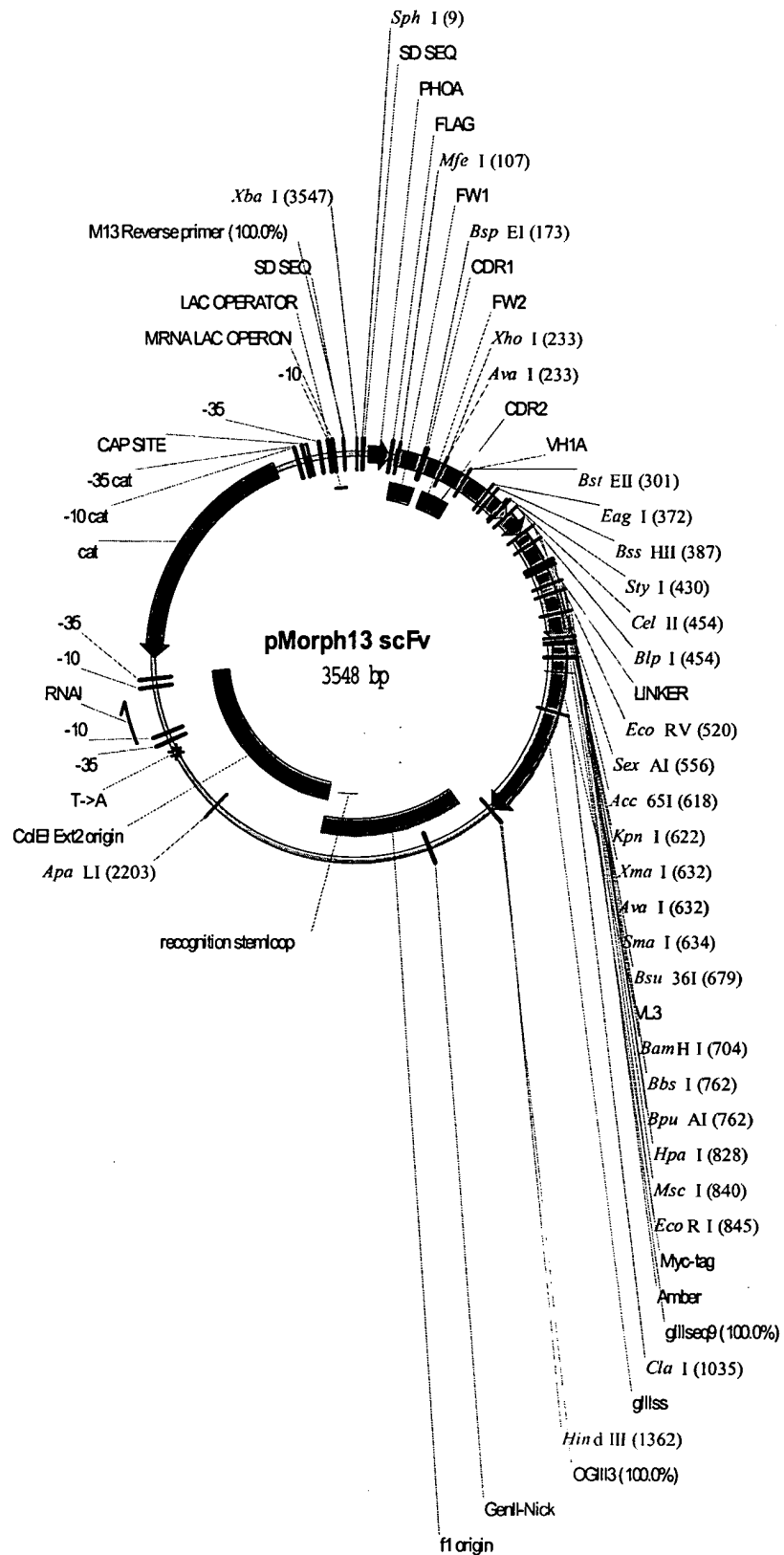


**mAb: 1D09C3**

Figure 10



# Figure 11



TO5TFT"4E6T000T

## Figure 11 (cont.)

XbaISphI

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1 AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC  
TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG

51 ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG  
TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC

MfeI

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101 AAGTGCAATT GGTTCACTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC  
TTCACGTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTTGG CCCGTCGTCG

BspEI

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151 GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT  
CACTTTCCT CGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA

XhoI

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AvaI

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201 TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA  
ATCGACCCAC GCGGTTCTGG GACCCGTCCC AGAGCTCACC TACCCGCCGT

BstEII

~

251 TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG  
AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC

BstEII

~~~~~

301 GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAAGTGA  
CACTGGTAAT GGCGCCTACT TTCGTGGTGC TGGCGCATAT ACCTTGACTC

EagI

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BssHII

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351 CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG  
GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC

StyI

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401 ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT  
TAGCATACAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA

BlpI

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CelII

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451 AGCTCAGCGG GTGGCGGTTC TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC  
TCGAGTCGCC CACCGCCAAG ACCGCCGCCA CCCTCGCCAC CGCCACCAAG

EcoRV

~~~~~

501 TGGCGGTGGT GGTTCCGATA TCGAACTGAC CCAGCCGCCT TCAGTGAGCG



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    GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAAATT

1151 TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTGAATGT
    ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1201 CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
    GCGGGAAAAC AGAAACCGCG ACCATTGTTG ATACTTAAAA GATAACTAAC

1251 TGACAAAATA AACTTATTCC GTGGTGTCTT TCGTTTTCTT TTATATGTTG
    ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1301 CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG
    GGTGGAAATA CATAcataaa AGATGCAAAC GATTGTATGA CGCATTATTC

                                HindIII
                                ~~~~~~
1351 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
    CTCAGAACTA TTCGAAC TGG ACACCTTCACT TTTTACCGCG TCTAACACGC
                                OGIII3 100.0%
                                =====

1401 ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACGTT AATATTTTGT
    TGTAACAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAACA

1451 TAAAATTCGC GTTAAATTTT TGTTAAATCA GTCATTTTTT TAACCAATAG
    ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

1501 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
    CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

1551 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
    CAACTCACAA CAAGGTCAAA CCTGTCTCTC AGGTGATAAT TTCTTGACCC

1601 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
    TGAGGTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

1651 CGAGAACCAT CACCCTAATC AAGTTTTTTTG GGGTCGAGGT GCCGTAAAGC
    GCTCTTGTA GTGGGATTAG TTCAAAAAC CCCAGCTCCA CGGCATTTTC

1701 ACTAAATCGG AACCTTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
    TGATTTAGCC TTGGGATTTT CCTCGGGGGC TAAATCTCGA ACTGCCCTT

1751 AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
    TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCC

1801 GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
    CGATCCCGCG ACCGTTTACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

1851 CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
    GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT AACTCGTTT

1901 AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
    TCCGGTCGTT TTCCGGTCTT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

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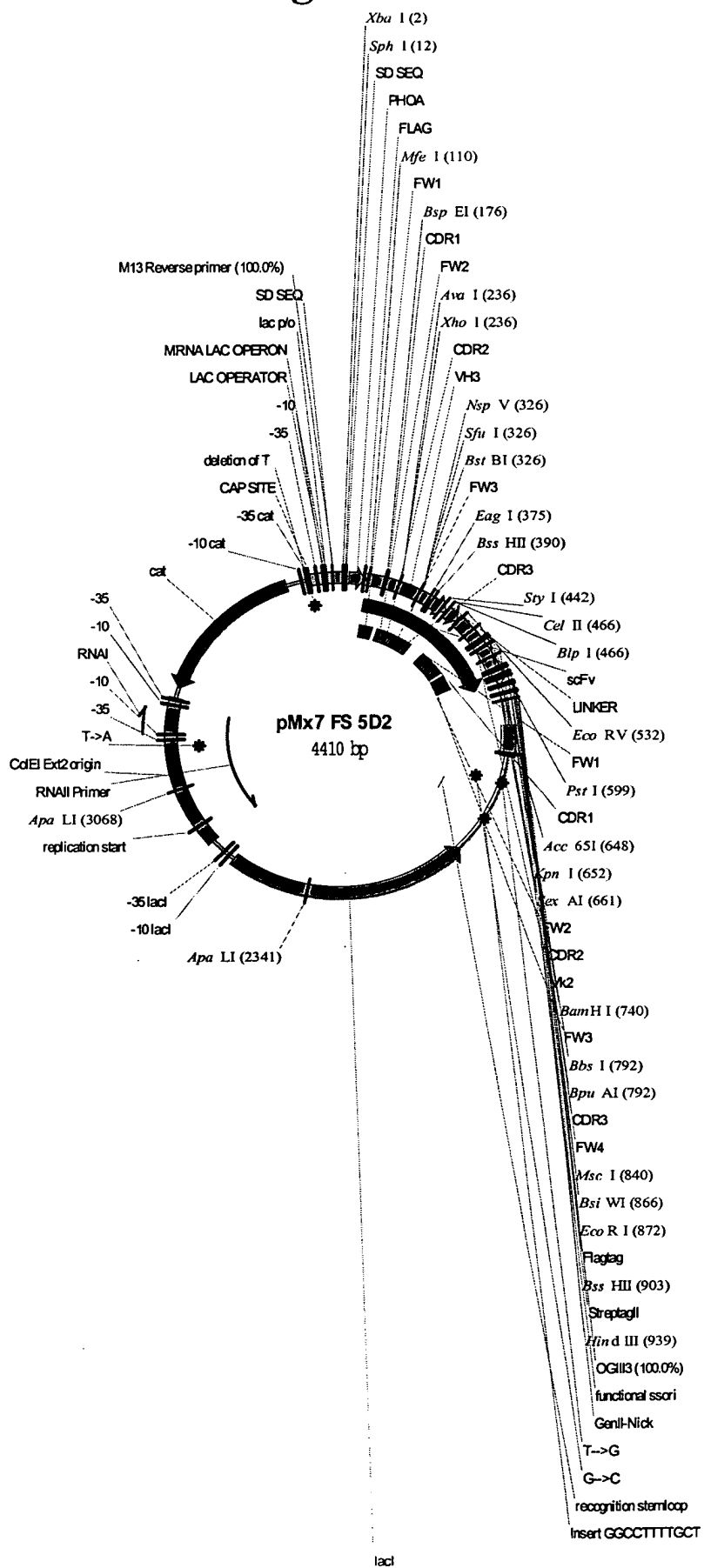
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2051	TGGAAGCTCC	CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	CTTACCGGAT
	ACCTTCGAGG	GAGCACGCGA	GAGGACAAGG	CTGGGACGGC	GAATGGCCTA
2101	ACCTGTCCGC	CTTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	TCATAGCTCA
	TGGACAGGCG	GAAAGAGGGA	AGCCCTTCGC	ACCGCGAAAG	AGTATCGAGT
2151	CGCTGTAGGT	ATCTCAGTTC	GGTGTAGGTC	GTTGCTCCA	AGCTGGGCTG
	GCGACATCCA	TAGAGTCAAG	CCACATCCAG	CAAGCGAGGT	TCGACCCGAC
	ApaLI				
	~~~~~				
2201	TGTGCACGAA	CCCCCGTTC	AGTCCGACCG	CTGCGCCTTA	TCCGGTAACT
	ACACGTGCTT	GGGGGGCAAG	TCAGGCTGGC	GACGCGGAAT	AGGCCATTGA
2251	ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	ACTGGCAGCA
	TAGCAGAACT	CAGGTTGGGC	CATTCTGTGC	TGAATAGCGG	TGACCGTCGT
2301	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	TATGTAGGCG	GTGCTACAGA
	CGGTGACCAT	TGTCCTAATC	GTCTCGCTCC	ATACATCCGC	CACGATGTCT
2351	GTTCTTGAAG	TGGTGGCCTA	ACTACGGCTA	CACTAGAAGA	ACAGTATTTG
	CAAGAACTTC	ACCACCGGAT	TGATGCCGAT	GTGATCTTCT	TGTCATAAAC
2401	GTATCTGCGC	TCTGCTGTAG	CCAGTTACCT	TCGGAAAAAG	AGTTGGTAGC
	CATAGACGCG	AGACGACATC	GGTCAATGGA	AGCCTTTTTT	TCAACCATCG
2451	TCTTGATCCG	GCAAACAAAC	CACCGCTGGT	AGCGGTGGTT	TTTTTGTTTG
	AGAACTAGGC	CGTTTGTTTG	GTGGCGACCA	TCGCCACCAA	AAAAACAAAC
2501	CAAGCAGCAG	ATTACGCGCA	GAAAAAAAGG	ATCTCAAGAA	GATCCTTTGA
	GTTGCTCGTC	TAATGCGCGT	CTTTTTTTCC	TAGAGTTCTT	CTAGGAAACT
2551	TCTTTTCTAC	GGGGTCTGAC	GCTCAGTGGA	ACGAAAACCT	ACGTTAAGGG
	AGAAAAGATG	CCCCAGACTG	CGAGTCACCT	TGCTTTTGAG	TGCAATTCCC
2601	ATTTTGGTCA	GATCTAGCAC	CAGGCGTTTA	AGGGCACCAA	TAAGTGCCTT
	TAAAACCACT	CTAGATCGTG	GTCCGCAAT	TCCCGTGGTT	ATTGACGGAA
2651	AAAAAAATTA	CGCCCCGCC	TGCCACTCAT	CGCAGTACTG	TTGTAATTCA
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2701	TTAAGCATTC	TGCCGACATG	GAAGCCATCA	CAAACGGCAT	GATGAACCTG
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2751	AATCGCCAGC	GGCATCAGCA	CCTTGTCGCC	TTGCGTATAA	TATTTGCCCA
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2801	TAGTGAAAAC	GGGGGCGAAG	AAGTTGTCCA	TATTGGCTAC	GTTTAAATCA
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2851	AAACTGGTGA	AACTCACCCA	GGGATTGGCT	GAGACGAAAA	ACATATTCTC
	TTTGACCACT	TTGAGTGGGT	CCCTAACCGA	CTCTGCTTTT	TGTATAAGAG

2901	AATAAACCTT	TTAGGGAAAT	AGGCCAGGTT	TTCACCGTAA	CACGCCACAT
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3051	GTGAACACTA	TCCCATATCA	CCAGCTCACC	GTCTTTCATT	GCCATACGGA
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3101	ACTCCGGGTG	AGCATTTCATC	AGGCGGGCAA	GAATGTGAAT	AAAGGCCGGA
	TGAGGCCAC	TCGTAAGTAG	TCCGCCCGTT	CTTACACTTA	TTTCCGGCCT
3151	TAAAACTTGT	GCTTATTTTT	CTTTACGGTC	TTTAAAAAGG	CCGTAATATC
	ATTTTGAACA	CGAATAAAAA	GAAATGCCAG	AAATTTTTCC	GGCATTATAG
3201	CAGCTGAACG	GTCTGGTTAT	AGGTACATTG	AGCAACTGAC	TGAAATGCCT
	GTCGACTTGC	CAGACCAATA	TCCATGTAAC	TCGTTGACTG	ACTTTACGGA
3251	CAAAATGTTC	TTTACGATGC	CATTGGGATA	TATCAACGGT	GGTATATCCA
	GTTTTACAAG	AAATGCTACG	GTAACCCTAT	ATAGTTGCCA	CCATATAGGT
3301	GTGATTTTTT	TCTCCATTTT	AGCTTCCTTA	GCTCCTGAAA	ATCTCGATAA
	CACTAAAAAA	AGAGGTAAAA	TCAAGGAAT	CGAGGACTTT	TAGAGCTATT
3351	CTCAAAAAAT	ACGCCCCGTA	GTGATCTTAT	TTCATTATGG	TGAAAGTTGG
	GAGTTTTTTA	TGCGGGCCAT	CACTAGAATA	AAGTAATACC	ACTTTCAACC
3401	AACCTCACCC	GACGTCTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCAG
	TTGGAGTGGG	CTGCAGATTA	CACTCAATCG	AGTGAGTAAT	CCGTGGGGTC
3451	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	TTGTGTGGAA	TTGTGAGCGG
	CGAAATGTGA	AATACGAAGG	CCGAGCATAC	AACACACCTT	AACACTCGCC
		M13 Reverse primer 100.0%		XbaI	
		=====		~~	
3501	ATAACAATTT	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATTTCT
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210019543103



## Figure 12 (cont)

XbaI SphI

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1 TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT  
AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

51 GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG  
CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

MfeI

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101 ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC  
TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG

BspEI

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151 AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC  
TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG

XhoI

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AvaI

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201 GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG  
CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC

251 CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC  
GCTAATCGCC ATCGCCGCCG TCGTGGATAA TACGCCTATC GCACTTTCCG

BstBI

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SfuI

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NspV

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301 CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT  
GCAAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA

EagI

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BssHII

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351 GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA  
CTTGTCGGAC GCACGCCTTC TATGCCGCA CATAATAACG CGCGCACAAAT

StyI

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401 AGAAGCATTT TTCTCGTAAG AATTGGTTTG ATTATTGGGG CCAAGGCACC  
TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTCCGTGG

BlpI

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CelII

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451 CTGGTGACGG TTAGCTCAGC GGGTGGCGGT TCTGGCGGCG GTGGGAGCGG  
GACCACTGCC AATCGAGTCG CCCACCGCCA AGACCGCCGC CACCCTCGCC

EcoRV

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501 TGGCGGTGGT TCTGGCGGTG GTGGTTCCGA TATCGTGATG ACCCAGAGCC  
ACCGCCACCA AGACCGCCAC CACCAAGGCT ATAGCACTAC TGGGTCTCGG

PstI

~~~~~

551 CACTGAGCCT GCCAGTGA CTGGGCGAGC CTGCGAGCAT TAGCTGCAGA  
GTGACTCGGA CGGTCCTGTA GGCCCGCTCG GACGCTCGTA ATCGACGTCT

KpnI

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Acc65I

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601 AGCAGCCAAA GCCTGCTGCA TAGCAACGGC TATAACTATC TGGATTGGTA  
TCGTCGGTTT CGGACGACGT ATCGTTGCCG ATATTGATAG ACCTAACCAT

KpnI

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Acc65I

SexAI

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651 CCTTCAAAAA CCAGGTCAAA GCCCGCAGCT ATTAATTTAT CTGGGCAGCA  
GGAAGTTTTT GGTCCAGTTT CGGGCGTCGA TAATTAAATA GACCCGTCGT

BamHI

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701 ACCGTGCCAG TGGGGTCCCG GATCGTTTTA GCGGCTCTGG ATCCGGCACC  
TGGCACGGTC ACCCCAGGGC CTAGCAAAT CGCCGAGACC TAGGCCGTGG

BpuAI

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BbsI

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751 GATTTTACCC TGAAAATTAG CCGTGTGGAA GCTGAAGACG TGGGCGTGTA  
CTAAATGGG ACTTTTAATC GGCACACCTT CGACTTCTGC ACCCGCACAT

MscI

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801 TTATTGCCAG CAGCATTATA CCACCCCGCC GACCTTTGGC CAGGGTACGA  
AATAACGGTC GTCGTAATAT GGTGGGGCGG CTGGAAACCG GTCCCATGCT

10001934.11501



1501	TAGACTAGTG	TTTAAACCGG	ACCGGGGGGG	GGCTTAAGTG	GGCTGCAAAA
	ATCTGATCAC	AAATTTGGCC	TGGCCCCCCC	CCGAATTCAC	CCGACGTTTT
1551	CAAAACGGCC	TCCTGTCAGG	AAGCCGCTTT	TATCGGGTAG	CCTCACTGCC
	GTTTTGCCGG	AGGACAGTCC	TTGCGCGAAA	ATAGCCCATC	GGAGTGACGG
1601	CGCTTTCCAG	TCGGGAAACC	TGTCGTGCCA	GCTGCATCAG	TGAATCGGCC
	GCGAAAGGTC	AGCCCTTTGG	ACAGCACGGT	CGACGTAGTC	ACTTAGCCGG
1651	AACGCGCGGG	GAGAGGCGGT	TTGCGTATTG	GGAGCCAGGG	TGGTTTTTCT
	TTGCGCGCCC	CTCTCCGCCA	AACGCATAAC	CCTCGGTCCC	ACCAAAAAGA
1701	TTTCACCAGT	GAGACGGGCA	ACAGCTGATT	GCCCTTCACC	GCCTGGCCCT
	AAAGTGGTCA	CTCTGCCCCG	TGTCGACTAA	CGGGAAGTGG	CGGACCGGGA
1751	GAGAGAGTTG	CAGCAAGCGG	TCCACGCTGG	TTTGCCCCAG	CAGGCGAAAA
	CTCTCTCAAC	GTCGTTTCGC	AGGTGCGACC	AAACGGGGTC	GTCCGCTTTT
1801	TCCTGTTTGA	TGGTGGTCAG	CGGCGGGATA	TAACATGAGC	TGTCCTCGGT
	AGGACAAACT	ACCACCAGTC	GCCGCCCTAT	ATTGTACTCG	ACAGGAGCCA
1851	ATCGTCGTAT	CCCACTACCG	AGATGTCCGC	ACCAACGCGC	AGCCCGGACT
	TAGCAGCATA	GGGTGATGGC	TCTACAGGCG	TGGTTGCGCG	TCGGGCCTGA
1901	CGGTAATGGC	ACGCATTGCG	CCCAGCGCCA	TCTGATCGTT	GGCAACCAGC
	GCCATTACCG	TGCGTAACGC	GGGTGCGGGT	AGACTAGCAA	CCGTTGGTCG
1951	ATCGCAGTGG	GAACGATGCC	CTCATTCAGC	ATTTGCATGG	TTTGTTGAAA
	TAGCGTCACC	CTTGCTACGG	GAGTAAGTCG	TAAACGTACC	AAACAACTTT
2001	ACCGGACATG	GCACTCCAGT	CGCCTTCCCG	TTCCGCTATC	GGCTGAATTT
	TGGCCTGTAC	CGTGAGGTCA	GCGGAAGGGC	AAGGCGATAG	CCGACTTAAA
2051	GATTGCGAGT	GAGATATTTA	TGCCAGCCAG	CCAGACGCAG	ACGCGCCGAG
	CTAACGCTCA	CTCTATAAAT	ACGGTCGGTC	GGTCTGCGTC	TGCGCGGCTC
2101	ACAGAACTTA	ATGGGCCAGC	TAACAGCGCG	ATTTGCTGGT	GGCCCAATGC
	TGTCTTGAAT	TACCCGGTCG	ATTGTCGCGC	TAAACGACCA	CCGGGTACG
2151	GACCAGATGC	TCCACGCCCA	GTCGCGTACC	GTCCTCATGG	GAGAAAATAA
	CTGGTCTACG	AGGTGCGGGT	CAGCGCATGG	CAGGAGTACC	CTCTTTTATT
2201	TACTGTTGAT	GGGTGTCTGG	TCAGAGACAT	CAAGAAATAA	CGCCGGAACA
	ATGACAACTA	CCCACAGACC	AGTCTCTGTA	GTTCTTTATT	GCGGCCTTGT
2251	TTAGTGCAGG	CAGCTTCCAC	AGCAATAGCA	TCCTGGTCAT	CCAGCGGATA
	AATCACGTCC	GTCGAAGGTG	TCGTTATCGT	AGGACCAGTA	GGTCGCCTAT
				ApaLI	
				~~~~~	
2301	GTTAATAATC	AGCCCACTGA	CACGTTGCGC	GAGAAGATTG	TGCACCGCCG
	CAATTATTAG	TCGGGTGACT	GTGCAACGCG	CTCTTCTAAC	ACGTGGCGGC
2351	CTTTACAGGC	TTCGACGCCG	CTTCGTTCTA	CCATCGACAC	GACCACGCTG
	GAAATGTCCG	AAGCTGCGGC	GAAGCAAGAT	GGTAGCTGTG	CTGGTGCGAC

2401 GCACCCAGTT GATCGGCGCG AGATTTAATC GCCGCGACAA TTTGCGACGG  
CGTGGGTCAA CTAGCCGCGC TCTAAATTAG CGGCGCTGTT AAACGCTGCC

2451 CGCGTGCAGG GCCAGACTGG AGGTGGCAAC GCCAATCAGC AACGACTGTT  
GCGCACGTCC CGGTCTGACC TCCACCGTTG CGGTTAGTCG TTGCTGACAA

2501 TGCCCGCCAG TTGTTGTGCC ACGCGGTTAG GAATGTAATT CAGCTCCGCC  
ACGGGCGGTC AACAACACGG TGCGCCAATC CTTACATTAA GTCGAGGCGG

2551 ATCGCCGCTT CCACTTTTTTC CCGCGTTTTTC GCAGAAACGT GGCTGGCCTG  
TAGCGGCGAA GGTGAAAAAG GGCGCAAAAG CGTCTTTGCA CCGACCGGAC

2601 GTTCACCACG CGGGAAACGG TCTGATAAGA GACACCGGCA TACTCTGCGA  
CAAGTGGTGC GCCCTTTGCC AGACTATTCT CTGTGGCCGT ATGAGACGCT

2651 CATCGTATAA CGTTACTGGT TTCACATTCA CCACCCTGAA TTGACTCTCT  
GTAGCATATT GCAATGACCA AAGTGTAAGT GGTGGGACTT AACTGAGAGA

2701 TCCGGGCGCT ATCATGCCAT ACCGCGAAAG GTTTTGCGCC ATTCGATGCT  
AGGCCCGCGA TAGTACGGTA TGGCGCTTTC CAAAACGCGG TAAGCTACGA

2751 AGCCATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG  
TCGGTACACT CGTTTTCCGG TCGTTTTCCG GTCCTTGGA TTTTCCGGC

2801 CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA  
GCAACGACCG CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT

2851 AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA  
TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGCTGTCCTG ATATTTCTAT

2901 CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC  
GGTCCGCAA GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG

2951 TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG  
ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTCGCACCGC

3001 CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCTG  
GAAAGAGTAT CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC

ApaLI

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3051 CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC GACCGCTGCG  
GAGGTTGAC CCGACACACG TGCTTGGGGG GCAAGTCGGG CTGGCGACGC

3101 CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA  
GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTG TGTGCTGAAT

3151 TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT  
AGCGGTGACC GTCGTGCGTG ACCATTGTCC TAATCGTCTC GCTCCATACA

3201 AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA  
TCCGCCACGA TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT

3251 GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGTAGCCAGT TACCTTCGGA  
CTTCTTGTC TAAACCATAG ACGCGAGACG ACATCGGTCA ATGGAAGCCT

|      |            |            |            |            |             |
|------|------------|------------|------------|------------|-------------|
| 3301 | AAAAGAGTTG | GTAGCTCTTG | ATCCGGCAAA | CAAACCACCG | CTGGTAGCGG  |
|      | TTTTCTCAAC | CATCGAGAAC | TAGGCCGTTT | GTTTGGTGGC | GACCATCGCC  |
| 3351 | TGGTTTTTTT | GTTTGCAAGC | AGCAGATTAC | GCGCAGAAAA | AAAGGATCTC  |
|      | ACCAAAAAAA | CAAACGTTTC | TCGTCTAATG | CGCGTCTTTT | TTTCCTAGAG  |
| 3401 | AAGAAGATCC | TTTGATCTTT | TCTACGGGGT | CTGACGCTCA | GTGGAACGAA  |
|      | TTCTTCTAGG | AAACTAGAAA | AGATGCCCCA | GACTGCGAGT | CACCTTGCTT  |
| 3451 | AACTCACGTT | AAGGGATTTT | GGTCAGATCT | AGCACCAGGC | GTTTAAGGGC  |
|      | TTGAGTGCAA | TTCCCTAAAA | CCAGTCTAGA | TCGTGGTCCG | CAAATTCCCC  |
| 3501 | ACCAATAACT | GCCTTAAAAA | AATTACGCCC | CGCCCTGCCA | CTCATCGCAG  |
|      | TGGTTATTGA | CGGAATTTTT | TTAATGCGGG | GCGGGACGGT | GAGTAGCGTC  |
| 3551 | TACTGTTGTA | ATTCATTAAG | CATTCTGCCG | ACATGGAAGC | CATCACAAAC  |
|      | ATGACAACAT | TAAGTAATTC | GTAAGACGGC | TGTACCTTCG | GTAGTGTTTG  |
| 3601 | GGCATGATGA | ACCTGAATCG | CCAGCGGCAT | CAGCACCTTG | TCGCCTTGCG  |
|      | CCGTACTACT | TGGACTTAGC | GGTCGCCGTA | GTCGTGGAAC | AGCGGAACGC  |
| 3651 | TATAATATTT | GCCCATAGTG | AAAACGGGGG | CGAAGAAGTT | GTCCATATTG  |
|      | ATATTATAAA | CGGGTATCAC | TTTTGCCCCC | GCTTCTTCAA | CAGGTATAAC  |
| 3701 | GCTACGTTTA | AATCAAAACT | GGTGAAACTC | ACCCAGGGAT | TGGCTGAGAC  |
|      | CGATGCAAAT | TTAGTTTTGA | CCACTTTGAG | TGGGTCCCTA | ACCGACTCTG  |
| 3751 | GAAAAACATA | TTCTCAATAA | ACCCTTTAGG | GAAATAGGCC | AGGTTTTTCAC |
|      | CTTTTTGTAT | AAGAGTTATT | TGGGAAATCC | CTTTATCCGG | TCCAAAAGTG  |
| 3801 | CGTAACACGC | CACATCTTGC | GAATATATGT | GTAGAAACTG | CCGGAAATCG  |
|      | GCATTGTGCG | GTGTAGAACG | CTTATATACA | CATCTTTGAC | GGCCTTTAGC  |
| 3851 | TCGTGGTATT | CACTCCAGAG | CGATGAAAAC | GTTTCAGTTT | GCTCATGGAA  |
|      | AGCACCATAA | GTGAGGTCTC | GCTACTTTTG | CAAAGTCAA  | CGAGTACCTT  |
| 3901 | AACGGTGTA  | CAAGGGTGAA | CACTATCCCA | TATCACCAGC | TCACCGTCTT  |
|      | TTGCCACATT | GTTCCCACTT | GTGATAGGGT | ATAGTGGTCG | AGTGGCAGAA  |
| 3951 | TCATTGCCAT | ACGGAACTCC | GGGTGAGCAT | TCATCAGGCG | GGCAAGAATG  |
|      | AGTAACGGTA | TGCCTTGAGG | CCCACTCGTA | AGTAGTCCGC | CCGTTCTTAC  |
| 4001 | TGAATAAAGG | CCGGATAAAA | CTTGTGCTTA | TTTTTCTTTA | CGGTCTTTAA  |
|      | ACTTATTTCC | GGCCTATTTT | GAACACGAAT | AAAAAGAAAT | GCCAGAAATT  |
| 4051 | AAAGGCCGTA | ATATCCAGCT | GAACGGTCTG | GTTATAGGTA | CATTGAGCAA  |
|      | TTTCCGGCAT | TATAGGTCGA | CTTGCCAGAC | CAATATCCAT | GTAACTCGTT  |
| 4101 | CTGACTGAAA | TGCCTCAAAA | TGTTCTTTAC | GATGCCATTG | GGATATATCA  |
|      | GACTGACTTT | ACGGAGTTTT | ACAAGAAATG | CTACGGTAAC | CCTATATAGT  |
| 4151 | ACGGTGGTAT | ATCCAGTGAT | TTTTTTCTCC | ATTTTAGCTT | CCTTAGCTCC  |
|      | TGCCACCATA | TAGGTCACTA | AAAAAGAGG  | TAAAATCGAA | GGAATCGAGG  |
| 4201 | TGAAAATCTC | GATAACTCAA | AAAATACGCC | CGGTAGTGAT | CTTATTTTCAT |
|      | ACTTTTAGAG | CTATTGAGTT | TTTTATGCGG | GCCATCACTA | GAATAAAGTA  |

4251 TATGGTGAAA GTTGGAACCT CACCCGACGT CTAATGTGAG TTAGCTCACT  
ATACCACTTT CAACCTTGGA GTGGGCTGCA GATTACACTC AATCGAGTGA

4301 CATTAGGCAC CCCAGGCTTT ACACCTTATG CTTCCGGCTC GTATGTTGTG  
GTAATCCGTG GGGTCCGAAA TGTGAAATAC GAAGGCCGAG CATAACAACAC

M13 Reverse primer 100.0%

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4351 TGGAATTGTG AGCGGATAAC AATTCACAC AGGAAACAGC TATGACCATG  
ACCTTAACAC TCGCCTATTG TTAAAGTGTG TCCTTTGTG ATACTGGTAC

4401 ATTACGAATT  
TAATGCTTAA

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# Figure 13 (cont)

|     |            |            |            |            |             |
|-----|------------|------------|------------|------------|-------------|
|     | EcoRV      |            |            |            | SexAI       |
|     | ~~~        |            |            |            | ~~~~~       |
| 1   | ATCGTGCTGA | CCCAGCCGCC | TTCAGTGAGT | GGCGCACCAG | GTCAGCGTGT  |
|     | TAGCACGACT | GGGTCGGCGG | AAGTCACTCA | CCGCGTGGTC | CAGTCGCACA  |
| 51  | GACCATCTCG | TGTAGCGGCA | GCAGCAGCAA | CATTGGCAGC | AACTATGTGA  |
|     | CTGGTAGAGC | ACATCGCCGT | CGTCGTCGTT | GTAACCGTCG | TTGATACTACT |
|     |            | XmaI       |            |            |             |
|     |            | ~~~~~      |            |            |             |
|     | KpnI       | SmaI       |            |            |             |
|     | ~~~~~      | ~~~~~      |            |            |             |
|     | Acc65I     | AvaI       |            |            |             |
|     | ~~~~~      | ~~~~~      |            |            |             |
| 101 | GCTGGTACCA | GCAGTTGCC  | GGGACGGCGC | CGAAACTGCT | GATTTATGAT  |
|     | CGACCATGGT | CGTCAACGGG | CCCTGCCGCG | GCTTTGACGA | CTAAATACTA  |
|     |            | Bsu36I     |            | BamHI      |             |
|     |            | ~~~~~      |            | ~~~~~      |             |
| 151 | AACAACCAGC | GTCCCTCAGG | CGTGCCGGAT | CGTTTTAGCG | GATCCAAAAG  |
|     | TTGTTGGTCG | CAGGGAGTCC | GCACGGCCTA | GCAAATCGC  | CTAGGTTTTT  |
|     |            |            |            | BpuAI      |             |
|     |            |            |            | ~~~~~      |             |
|     |            |            |            | BbsI       |             |
|     |            |            |            | ~~~~~      |             |
| 201 | CGGCACCAGC | GCGAGCCTTG | CGATTACGGG | CCTGCAAAGC | GAAGACGAAG  |
|     | GCCGTGGTCG | CGCTCGGAAC | GCTAATGCCC | GGACGTTTCG | CTTCTGCTTC  |
|     |            | Bsu36I     |            |            |             |
|     |            | ~~~~~      |            |            |             |
| 251 | CGGATTATTA | TTGCCAGAGC | TATGACATGC | CTCAGGCTGT | GTTTGCGCGC  |
|     | GCCTAATAAT | AACGGTCTCG | ATACTGTACG | GAGTCCGACA | CAAACCGCCG  |
|     |            | MscI       |            | DraIII     |             |
|     |            | ~~~~~      |            | ~~~~~      |             |
| 301 | GGCACGAAGT | TTAACCGTTC | TTGGCCAGCC | GAAAGCCGCA | CCGAGTGTGA  |
|     | CCGTGCTTCA | AATTGGCAAG | AACCGGTCGG | CTTTCGGCGT | GGCTCACACT  |
| 351 | CGCTGTTTCC | GCCGAGCAGC | GAAGAATTGC | AGGCGAACAA | AGCGACCCTG  |
|     | GCGACAAAGG | CGGCTCGTCG | CTTCTTAACG | TCCGCTTGTT | TCGCTGGGAC  |
| 401 | GTGTGCCTGA | TTAGCGACTT | TTATCCGGGA | GCCGTGACAG | TGGCCTGGAA  |
|     | CACACGGACT | AATCGCTGAA | AATAGGCCCT | CGGCACTGTC | ACCGGACCTT  |
| 451 | GGCAGATAGC | AGCCCCGTCA | AGGCGGGAGT | GGAGACCACC | ACACCCTCCA  |
|     | CCGTCTATCG | TCGGGGCAGT | TCCGCCCTCA | CCTCTGGTGG | TGTGGGAGGT  |
| 501 | AACAAAGCAA | CAACAAGTAC | GCGGCCAGCA | GCTATCTGAG | CCTGACGCCT  |
|     | TTGTTTCGTT | GTTGTTCATG | CGCCGGTCGT | CGATAGACTC | GGACTGCGGA  |
| 551 | GAGCAGTGGA | AGTCCCACAG | AAGCTACAGC | TGCCAGGTCA | CGCATGAGGG  |
|     | CTCGTCACCT | TCAGGGTGTC | TTCGATGTCT | ACGGTCCAGT | GCGTACTCCC  |

StuI

SphI

601 GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG  
CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGACT ATTCGTACGC

651 TAGGAGAAAA TAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG  
ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

MfeI

701 TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG  
AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTTAAC TTCTTTTCGC

BspEI

751 CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT  
GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

BspEI

801 CCGGATTTAG CCTGTCCACG TCTGGCGTTG GCGTGGGCTG GATTGCCCAG  
GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

XhoI

~~~~~

AvaI

~~~~~

851 CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA  
GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

901 TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA  
ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

BstBI

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SfuI

~~~~~

NspV

~~~~~

951 CTTCGAAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT  
GAAGCTTTTT AGTCCACCAC GACTGATACT GGTGTACCT GGGCCACCTA

BssHII

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1001 ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA  
TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAAC

BlpI

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StyI

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CelII

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1051 TTATTGGGGC CAAGGCACCC TGGTGACGGT TAGCTCAGCG TCGACCAAAG  
AATAACCCCG GTTCCGTGGG ACCACTGCCA ATCGAGTCGC AGCTGGTTTC

1101 GTCCAAGCGT GTTTCCGCTG GCTCCGAGCA GCAAAAGCAC CAGCGGCGGC  
CAGGTTTCGA CAAAGGCGAC CGAGGCTCGT CGTTTTCGTG GTCGCCGCCG

1151 ACGGCTGCCC TGGGCTGCCT GGTAAAGAT TATTTCCCGG AACCAGTCAC

1001934-11501

	TGCCGACGGG	ACCCGACGGA	CCAATTTCTA	ATAAAGGGCC	TTGGTCAGTG
1201	CGTGAGCTGG GCACTCGACC	AACAGCGGGG TTGTCGCCCC	CGCTGACCAG GCGACTGGTC	CGGCGTGCAT GCCGCACGTA	ACCTTTCGGG TGGAAGGCC
1251	CGGTGCTGCA GCCACGACGT	AAGCAGCGGC TTCGTCGCCG	CTGTATAGCC GACATATCGG	TGAGCAGCGT ACTCGTCGCA	TGTGACCGTG ACACTGGCAC
1301	CCGAGCAGCA GGCTCGTCGT	GCTTAGGCAC CGAATCCGTG	TCAGACCTAT AGTCTGGATA	ATTTGCAACG TAAACGTTGC	TGAACCATAA ACTTGGTATT
					EcoRI ~~~~~
1351	ACCGAGCAAC TGGCTCGTTG	ACCAAAGTGG TGGTTTCACC	ATAAAAAAGT TATTTTTTCA	GGAACCGAAA CCTTGGCTTT	AGCGAATTCG TCGCTTAAGC
			BssHII ~~~~~		
1401	ACTATAAAGA TGATATTTCT	TGACGATGAC ACTGCTACTG	AAAGGCGCGC TTTCCGCGCG	CGTGGAGCCA GCACCTCGGT	CCCGCAGTTT GGGCGTCAAA
		HindIII ~~~~~			
1451	GAAAAATGAT CTTTTTACTA	AAGCTTGACC TTCGAACTGG	TGTGAAGTGA ACACTTCACT	AAAATGGCGC TTTTACCGCG	AGATTGTGCG TCTAACACGC
			OGIII3 100.0%		
			=====		
1501	ACATTTTTTT TGTAACAAAA	TGTCTGCCGT ACAGACGGCA	TTAATTAAAG AATTAATTTT	GGGGGGGGGG CCCCCCCCC	GCCGGCCTGG CGGCCGGACC
1551	GGGGGGGTGT CCCCCCCACA	ACATGAAATT TGTACTTTAA	GTAAACGTTA CATTTGCAAT	ATATTTTGTG TATAAAACAA	AAAATTTCGG TTTTAAGCGC
1601	TTAAATTTTT AATTTAAAAA	GTTAAATCAG CAATTTAGTC	CTCATTTTTT GAGTAAAAAA	AACCAATAGG TTGGTTATCC	CCGAAATCGG GGCTTTAGCC
1651	CAAAATCCCT GTTTTAGGGA	TATAAATCAA ATATTTAGTT	AAGAATAGAC TTCTTATCTG	CGAGATAGGG GCTCTATCCC	TTGAGTGTTG AACTCACAA
1701	TTCCAGTTTG AAGGTCAAAC	GAACAAGAGT CTTGTTCTCA	CCACTATTAA GGTGATAATT	AGAACGTGGA TCTTGACCTT	CTCCAACGTC GAGGTTGCAG
1751	AAAGGGCGAA TTTCCCGCTT	AAACCGTCTA TTTGGCAGAT	TCAGGGCGAT AGTCCCGCTA	GGCCCACTAC CCGGGTGATG	GAGAACCATC CTCTTGGTAG
1801	ACCCTAATCA TGGGATTAGT	AGTTTTTTTG TCAAAAAACC	GGTCGAGGTG CCAGCTCCAC	CCGTAAAGCA GGCATTTCGT	CTAAATCGGA GATTTAGCCT
1851	ACCCTAAAGG TGGGATTTC	GAGCCCCCGA CTCGGGGGCT	TTTAGAGCTT AAATCTCGAA	GACGGGGAAA CTGCCCCTTT	GCCGGCGAAC CGGCCGCTTG
1901	GTGGCGAGAA CACCGCTCTT	AGGAAGGGAA TCCTTCCCTT	GAAAGCGAAA CTTTCGCTTT	GGAGCGGGCG CCTCGCCCGC	CTAGGGCGCT GATCCCGCGA
1951	GGCAAGTGTA CCGTTTACAT	GCGGTCACGC CGCCAGTGCG	TGCGCGTAAC ACGCGCATTG	CACCACACCC GTGGTGTGGG	GCCGCGCTTA CGGCGCGAAT

EcoRI

BsSHII

HindIII

OGIII3 100.0%

2001 ATGCGCCGCT ACAGGGCGCG TGCTAGACTA GTGTTTAAAC CGGACCGGGG  
TACGCGGCGA TGTCCCGCGC ACATCTGAT CACAAATTTG GCCTGGCCCC

2051 GGGGGCTTAA GTGGGCTGCA AAACAAAACG GCCTCCTGTC AGGAAGCCGC  
CCCCGAATT CACCCGACGT TTTGTTTTGC CGGAGGACAG TCCTTCGGCG

2101 TTTTATCGGG TAGCCTCACT GCGCGCTTTC CAGTCGGGAA ACCTGTCGTG  
AAAATAGCCC ATCGGAGTGA CGGGCGAAAG GTCAGCCCTT TGGACAGCAC

2151 CCAGCTGCAT CAGTGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCCTA  
GGTCGACGTA GTCACCTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT

2201 TTGGGAGCCA GGGTGGTTTT TCTTTTCACC AGTGAGACGG GCAACAGCTG  
AACCTTCGGT CCCACCAAAA AGAAAAGTGG TCACTCTGCC CGTTGTCGAC

2251 ATTGCCCTTC ACCGCCTGGC CCGAGAGAG TTGCAGCAAG CGGTCCACGC  
TAACGGGAAG TGGCGGACCG GGACTCTCTC AACGTCGTTC GCCAGGTGCG

2301 TGGTTTGCCC CAGCAGGCGA AAATCCTGTT TGATGGTGGT CAGCGGCGGG  
ACCAAACGGG GTCGTCCGCT TTTAGGACAA ACTACCACCA GTCGCGCGCC

2351 ATATAACATG AGCTGTCCTC GGTATCGTCG TATCCCACTA CCGAGATGTC  
TATATTGTAC TCGACAGGAG CCATAGCAGC ATAGGGTGAT GGCTCTACAG

2401 CGCACCAACG CGCAGCCCGG ACTCGGTAAT GGCACGCATT GCGCCAGCG  
GCGTGGTTGC GCGTCGGGCC TGAGCCATTA CCGTGCGTAA CGCGGGTCGC

2451 CCATCTGATC GTTGGCAACC AGCATCGCAG TGGGAACGAT GCCCTCATTC  
GGTAGACTAG CAACCGTTGG TCGTAGCGTC ACCCTTGCTA CGGGAGTAAG

2501 AGCATTTGCA TGGTTTGTTG AAAACCGGAC ATGGCACTCC AGTCGCCTTC  
TCGTAAACGT ACCAAACAAC TTTTGGCCTG TACCGTGAGG TCAGCGGAAG

2551 CCGTTCCGCT ATCGGCTGAA TTTGATTGCG AGTGAGATAT TTATGCCAGC  
GGCAAGGCGA TAGCCGACTT AACTAACGC TCACTCTATA AATACGGTCG

2601 CAGCCAGACG CAGACGCGCC GAGACAGAAC TTAATGGGCC AGCTAACAGC  
GTCGGTCTGC GTCTGCGCGG CTCTGTCTTG AATTACCCGG TCGATTGTGC

2651 GCGATTTGCT GGTGGCCCAA TGCGACCAGA TGCTCCACGC CCAGTCGCGT  
CGCTAAACGA CCACCGGGTT ACGCTGGTCT ACGAGGTGCG GGTCAGCGCA

2701 ACCGTCCTCA TGGGAGAAAA TAATACTGTT GATGGGTGTC TGGTCAGAGA  
TGGCAGGAGT ACCCTCTTTT ATTATGACAA CTACCCACAG ACCAGTCTCT

2751 CATCAAGAAA TAACGCCGGA ACATTAGTGC AGGCAGCTTC CACAGCAATA  
GTAGTTCTTT ATTGCGGCCT TGTAATCACG TCCGTCGAAG GTGTCGTTAT

2801 GCATCCTGGT CATCCAGCGG ATAGTTAATA ATCAGCCAC TGACACGTTG  
CGTAGGACCA GTAGGTCGCC TATCAATTAT TAGTCGGGTG ACTGTGCAAC

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2851 CGCGAGAAGA TTGTGCACCG CCGCTTTACA GGCTTCGACG CCGCTTCGTT  
GCGCTCTTCT AACACGTGGC GGCGAAATGT CCGAAGCTGC GGCGAAGCAA

|      |            |             |            |            |            |
|------|------------|-------------|------------|------------|------------|
| 2901 | CTACCATCGA | CACGACCACG  | CTGGCACCCA | GTTGATCGGC | GCGAGATTTA |
|      | GATGGTAGCT | GTGCTGGTGC  | GACCGTGGGT | CAACTAGCCG | CGCTCTAAAT |
| 2951 | ATCGCCGCGA | CAATTTGCGA  | CGGCGCGTGC | AGGGCCAGAC | TGGAGGTGGC |
|      | TAGCGGCGCT | GTTAAACGCT  | GCCGCGCACG | TCCCGGTCTG | ACCTCCACCG |
| 3001 | AACGCCAATC | AGCAACGACT  | GTTTGCCCGC | CAGTTGTTGT | GCCACGCGGT |
|      | TTGCGGTTAG | TCGTTGCTGA  | CAAACGGGCG | GTCAACAACA | CGGTGCGCCA |
| 3051 | TAGGAATGTA | ATTCAGCTCC  | GCCATCGCCG | CTTCCACTTT | TTCCCGCGTT |
|      | ATCCTTACAT | TAAGTCGAGG  | CGGTAGCGGC | GAAGGTGAAA | AAGGGCGCAA |
| 3101 | TTCGCAGAAA | CGTGGCTGGC  | CTGGTTCACC | ACGCGGAAAA | CGGTCTGATA |
|      | AAGCGTCTTT | GCACCGACCG  | GACCAAGTGG | TGCGCCCTTT | GCCAGACTAT |
| 3151 | AGAGACACCG | GCATACTCTG  | CGACATCGTA | TAACGTTACT | GGTTTCACAT |
|      | TCTCTGTGGC | CGTATGAGAC  | GCTGTAGCAT | ATTGCAATGA | CCAAAGTGTA |
| 3201 | TCACCACCTT | GAATTGACTC  | TCTTCCGGGC | GCTATCATGC | CATACCGCGA |
|      | AGTGGTGGGA | CTTAACTGAG  | AGAAGGCCCG | CGATAGTACG | GTATGGCGCT |
| 3251 | AAGGTTTTGC | GCCATTTCGAT | GCTAGCCATG | TGAGCAAAAG | GCCAGCAAAA |
|      | TTCCAAAACG | CGGTAAGCTA  | CGATCGGTAC | ACTCGTTTTT | CGGTGTTTTT |
| 3301 | GGCCAGGAAC | CGTAAAAAGG  | CCGCGTTGCT | GGCGTTTTTC | CATAGGCTCC |
|      | CCGGTCCCTG | GCATTTTTTC  | GGCGCAACGA | CCGCAAAAAG | GTATCCGAGG |
| 3351 | GCCCCCTGA  | CGAGCATCAC  | AAAAATCGAC | GCTCAAGTCA | GAGGTGGCGA |
|      | CGGGGGGACT | GCTCGTAGTG  | TTTTTAGCTG | CGAGTTCAGT | CTCCACCGCT |
| 3401 | AACCCGACAG | GACTATAAAG  | ATACCAGGCG | TTTCCCCCTG | GAAGCTCCCT |
|      | TTGGGCTGTC | CTGATATTTT  | TATGGTCCGC | AAAGGGGGAC | CTTCGAGGGA |
| 3451 | CGTGCGCTCT | CCTGTTCCGA  | CCCTGCCGCT | TACCGGATAC | CTGTCCGCCT |
|      | GCACGCGAGA | GGACAAGGCT  | GGGACGGCGA | ATGGCCTATG | GACAGGCGGA |
| 3501 | TTCTCCCTTC | GGGAAGCGTG  | GCGCTTTCTC | ATAGCTCACG | CTGTAGGTAT |
|      | AAGAGGGAAG | CCCTTCGCAC  | CGCGAAAGAG | TATCGAGTGC | GACATCCATA |

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3551	CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	TGCACGAACC
	GAGTCAAGCC	ACATCCAGCA	AGCGAGGTTC	GACCCGACAC	ACGTGCTTGG
3601	CCCCGTTCAG	CCCGACCGCT	GCGCCTTATC	CGGTAACAT	CGTCTTGAGT
	GGGGCAAGTC	GGGCTGGCGA	CGCGGAATAG	GCCATTGATA	GCAGAACTCA
3651	CCAACCCGGT	AAGACACGAC	TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC
	GGTTGGGCCA	TTCTGTGCTG	AATAGCGGTG	ACCGTCGTCT	GTGACCATTG
3701	AGGATTAGCA	GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG
	TCCTAATCGT	CTCGCTCCAT	ACATCCGCCA	CGATGTCTCA	AGAACTTCAC
3751	GTGGCCTAAC	TACGGCTACA	CTAGAAGAAC	AGTATTTGGT	ATCTGCGCTC
	CACCGGATTG	ATGCCGATGT	GATCTTCTTG	TCATAAACCA	TAGACGCGAG
3801	TGCTGTAGCC	AGTTACCTTC	GGAAAAAGAG	TTGGTAGCTC	TTGATCCGGC

	ACGACATCGG	TCAATGGAAG	CCTTTTTTCTC	AACCATCGAG	AACTAGGCCG
3851	AAACAAACCA TTTGTTTGGT	CCGCTGGTAG GGCGACCATC	CGGTGGTTTT GCCACCAAAA	TTTGTTTGCA AAACAAACGT	AGCAGCAGAT TCGTCTGTCTA
3901	TACGCGCAGA ATGCGCGTCT	AAAAAAGGAT TTTTTTCCTA	CTCAAGAAGA GAGTTCCTCT	TCCTTTGATC AGGAAACTAG	TTTTCTACGG AAAAGATGCC
3951	GGTCTGACGC CCAGACTGCG	TCAGTGGAAC AGTCACCTTG	GAAAACCTCAC CTTTTGAGTG	GTTAAGGGAT CAATTCCTTA	TTTGGTCAGA AAACCAGTCT
4001	TCTAGCACCA AGATCGTGGT	GGCGTTTAAG CCGCAAATTC	GGCACCAATA CCGTGGTTAT	ACTGCCTTAA TGACGGAATT	AAAAATTACG TTTTTAATGC
4051	CCCCGCCCTG GGGGCGGGAC	CCACTCATCG GGTGAGTAGC	CAGTACTGTT GTCATGACAA	GTAATTCATT CATTAAGTAA	AAGCATTCTG TTCGTAAGAC
4101	CCGACATGGA GGCTGTACCT	AGCCATCACA TCGGTAGTGT	AACGGCATGA TTGCCGTACT	TGAACCTGAA ACTTGGACTT	TCGCCAGCGG AGCGGTGCC
4151	CATCAGCACC GTAGTCGTGG	TTGTCGCCTT AACAGCGGAA	GCGTATAATA CGCATATTAT	TTTGCCCATA AAACGGGTAT	GTGAAAACGG CACTTTTGCC
4201	GGGCGAAGAA CCCGCTTCTT	GTTGTCCATA CAACAGGTAT	TTGGCTACGT AACCGATGCA	TTAAATCAAA AATTTAGTTT	ACTGGTGAAA TGACCACTTT
4251	CTCACCAGG GAGTGGGTCC	GATTGGCTGA CTAACCGACT	GACGAAAAAC CTGCTTTTTG	ATATTCTCAA TATAAGAGTT	TAAACCCTTT ATTTGGGAAA
4301	AGGGAAATAG TCCCTTTATC	GCCAGGTTTT CGGTCCAAAA	CACCGTAACA GTGGCATTGT	CGCCACATCT GCGGTGTAGA	TGCGAATATA ACGCTTATAT
4351	TGTGTAGAAA ACACATCTTT	CTGCCGGAAG GACGGCCTTT	TCGTCGTGGT AGCAGCACCA	ATCACTCCA TAAGTGAGGT	GAGCGATGAA CTCGCTACTT
4401	AACGTTTCAG TTGCAAAGTC	TTTGCTCATG AAACGAGTAC	GAAAACGGTG CTTTTGCCAC	TAACAAGGGT ATTGTTCCCA	GAACACTATC CTTGTGATAG
4451	CCATATCACC GGTATAGTGG	AGCTCACCGT TCGAGTGGCA	CTTTCATTGC GAAAGTAACG	CATACGGAAC GTATGCCTTG	TCCGGGTGAG AGGCCCACTC
4501	CATTTCATCAG GTAAGTAGTC	GCGGGCAAGA CGCCCGTTCT	ATGTGAATAA TACACTTATT	AGGCCGATA TCCGGCCTAT	AAACTTGTGC TTTGAACACG
4551	TTATTTTTCT AATAAAAAGA	TTACGGTCTT AATGCCAGAA	TAAAAAGGCC ATTTTCCGG	GTAATATCCA CATTATAGGT	GCTGAACGGT CGACTTGCCA
4601	CTGGTTATAG GACCAATATC	GTACATTGAG CATGTAATCT	CAACTGACTG GTTGACTGAC	AAATGCCTCA TTTACGGAGT	AAATGTTCTT TTTACAAGAA
4651	TACGATGCCA ATGCTACGGT	TTGGGATATA AACCCTATAT	TCAACGGTGG AGTTGCCACC	TATATCCAGT ATATAGGTCA	GATTTTTTTC CTAAAAAAG
4701	TCCATTTTAG AGGTAAATC	CTTCCTTAGC GAAGGAATCG	TCCTGAAAAT AGGACTTTTA	CTCGATAACT GAGCTATTGA	CAAAAAATAC GTTTTTTATG
4751	GCCCGGTAGT	GATCTTATTT	CATTATGGTG	AAAGTTGGAA	CCTCACCCGA

CGGGCCATCA CTAGAATAAA GTAATACCAC TTTCAACCTT GGAGTGGGCT

4801 CGTCTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT  
GCAGATTACA CTCAATCGAG TGAGTAATCC GTGGGGTCCG AAATGTGAAA

4851 ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT AACAAATTTCA  
TACGAAGGCC GAGCATACAA CACACCTTAA CACTCGCCTA TTGTTAAAGT

M13 Reverse primer 100.0% XbaI

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4901 CACAGGAAAC AGCTATGACC ATGATTACGA ATTTCTAGAT AACGAGGGCA  
GTGTCCTTTG TCGATACTGG TACTAATGCT TAAAGATCTA TTGCTCCCGT

4951 AAAAATGAAA AAGACAGCTA TCGCGATTGC AGTGGCACTG GCTGGTTTCG  
TTTTTACTTT TTCTGTCGAT AGCGCTAACG TCACCGTGAC CGACCAAAGC

EcoRV

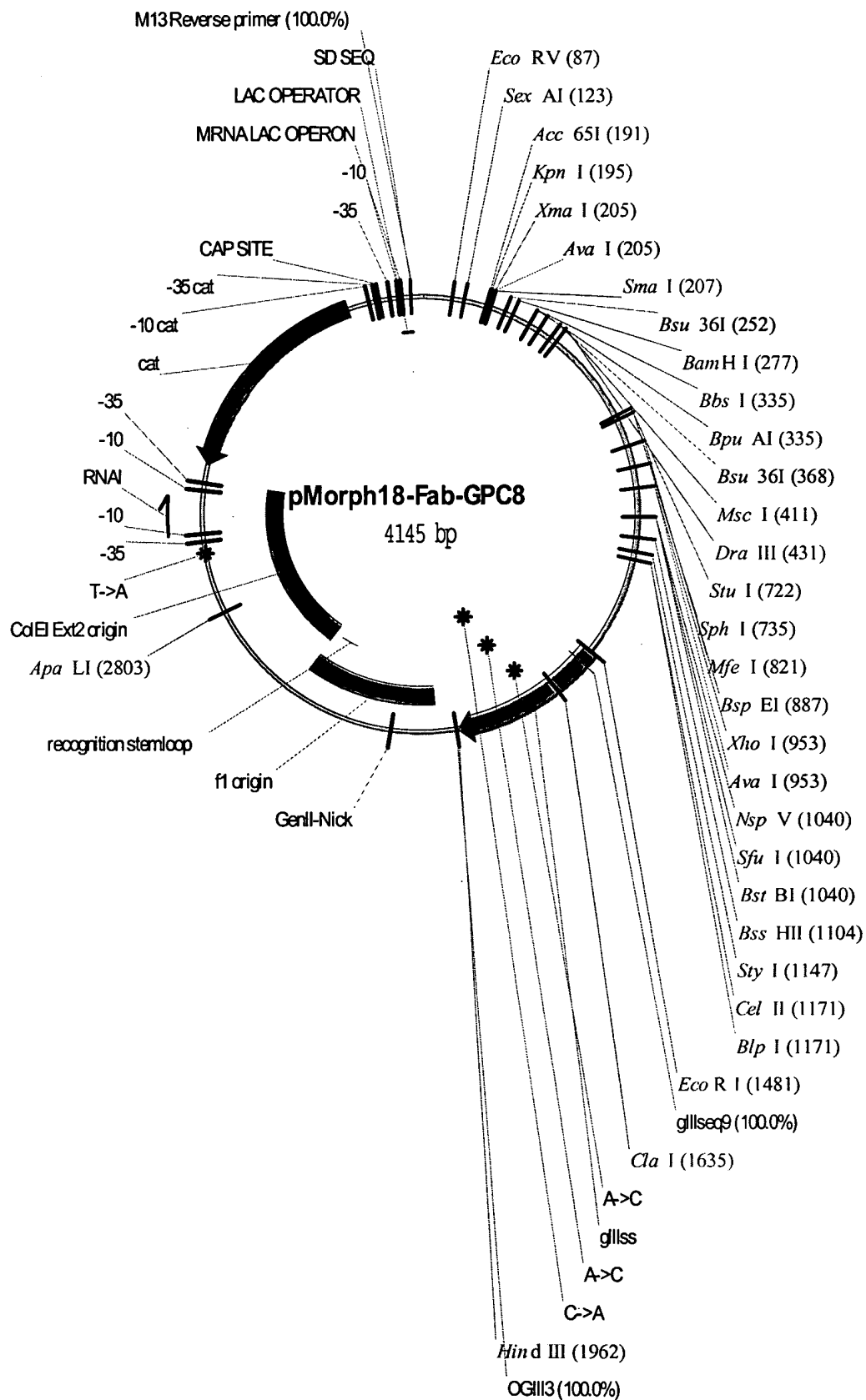
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5001 CTACCGTAGC GCAGGCCGAT  
GATGGCATCG CGTCCGGCTA

POST "46T00T"



# Figure 14



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## Figure 14 (cont)

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1  TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG
   AGTCTATTGC TCCCGTTTTT TACTTTTTCT GTCGATAGCG CTAACGTCAC

                                     EcoRV
                                     ~~~~~~
51  GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA
   CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT

                                     SexAI
                                     ~~~~~~
101 GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA
   CGGCGGAAGT CACTCACCGC GTGGTCCAGT CGCACACTGG TAGAGCACAT

                                     KpnI
                                     ~~~~~~
                                     Acc65I
                                     ~~~~~~
151 GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG
   CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC

   XmaI
   ~~~~~~
   SmaI
   ~~~~~~
   AvaI
   ~~~~~~
                                     Bsu36I
                                     ~~~~~~
201 TTGCCCCGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC
   AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG

   Bsu36I
   ~~~~~~
                                     BamHI
                                     ~~~~~~
251 CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAAGCGGC ACCAGCGCGA
   GAGTCCGCAC GGCCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT

                                     BpuAI
                                     ~~~~~~
                                     BbsI
                                     ~~~~~~
301 GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC
   CGGAACGCTA ATGCCCCGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG

                                     Bsu36I
                                     ~~~~~~
351 CAGAGCTATG ACATGCCTCA GGCTGTGTTT GGCGGCGGCA CGAAGTTTAA
   GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT

   MscI
   ~~~~~~
                                     DraIII
                                     ~~~~~~
401 CCGTTCTTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTCCGCCG
   GGCAAGAACC GGTCCGCTTT CGGCGTGGCT CACACTGCGA CAAAGGCGGC

451 AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG
   TCGTCGCTTC TTAACGTCGG CTTGTTCGCG TGGGACCACA CGGACTAATC

501 CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC

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GCTGAAAATA GGCCCTCGGC ACTGTCACCG GACCTTCCGT CTATCGTCGG

551 CCGTCAAGGC GGGAGTGGAG ACCACCACAC CCTCCAAACA AAGCAACAAC  
GGCAGTTCCG CCCTCACCTC TGGTGGTGTG GGAGGTTTGT TTCGTTGTTG

601 AAGTACGCGG CCAGCAGCTA TCTGAGCCTG ACGCCTGAGC AGTGGAAGTC  
TTCATGCGCC GGTTCGTCGAT AGACTCGGAC TGCGGACTCG TCACCTTCAG

651 CCACAGAAGC TACAGCTGCC AGGTCACGCA TGAGGGGAGC ACCGTGGAAA  
GGTGTCTTCG ATGTCGACGG TCCAGTGCGT ACTCCCCTCG TGGCACCTTT

StuI SphI  
~~~~~

701 AAACCGTTGC GCCGACTGAG GCCTGATAAG CATGCGTAGG AGAAAATAAA  
TTTGGCAACG CGGCTGACTC CGGACTATTC GTACGCATCC TCTTTTATTT

751 ATGAAACAAA GCACTATTGC ACTGGCACTC TTACCGTTGC TCTTCACCCC  
TACTTTGTTT CGTGATAACG TGACCGTGAG AATGGCAACG AGAAGTGGGG

MfeI  
~~~~~

801 TGTTACCAAA GCCCAGGTGC AATTGAAAGA AAGCGGCCCG GCCCTGGTGA  
ACAATGGTTT CGGGTCCACG TTAACCTTCT TTCGCCGGGC CGGGACCACT

BspEI  
~~~~~

851 AACCGACCCA AACCTGACC CTGACCTGTA CCTTTTCCGG ATTTAGCCTG  
TTGGCTGGGT TTGGGACTGG GACTGGACAT GGAAAAGGCC TAAATCGGAC

901 TCCACGTCTG GCGTTGGCGT GGGCTGGATT CGCCAGCCGC CTGGGAAAGC  
AGGTGCAGAC CGCAACCGCA CCCGACCTAA GCGGTCGGCG GACCCTTTTCG

XhoI  
~~~~~

AvaI  
~~~~~

951 CCTCGAGTGG CTGGCTCTGA TTGATTGGGA TGATGATAAG TATTATAGCA  
GGAGCTCACC GACCGAGACT AACTAACCTT ACTACTATTC ATAATATCGT

BstBI  
~~~~~

SfuI  
~~~~~

NspV  
~~~~~

1001 CCAGCCTGAA AACGCGTCTG ACCATTAGCA AAGATACTTC GAAAAATCAG  
GGTCGGACTT TTGCGCAGAC TGGTAATCGT TTCTATGAAG CTTTTTAGTC

1051 GTGGTGCTGA CTATGACCAA CATGGACCCG GTGGATACGG CCACCTATTA  
CACCACGACT GATACTGGTT GTACCTGGGC CACCTATGCC GGTGGATAAT

BssHII StyI  
~~~~~

1101 TTGCGCGCGT TCTCCTCGTT ATCGTGGTGC TTTTGATTAT TGGGGCCAAG  
AACGCGCGCA AGAGGAGCAA TAGCACCACG AAAACTAATA ACCCCGGTTC

|      | StyI       |             | CellI      |            |             |
|------|------------|-------------|------------|------------|-------------|
|      | ~          |             | ~~~~~      |            |             |
| 1151 | GCACCTGGT  | GACGGTTAGC  | TCAGCGTCGA | CCAAAGGTCC | AAGCGTGT    |
|      | CGTGGGACCA | CTGCCAATCG  | AGTCGCAGCT | GGTTTCCAGG | TTCGCACAAA  |
| 1201 | CCGCTGGCTC | CGAGCAGCAA  | AAGCACCAGC | GGCGGCACGG | CTGCCCTGGG  |
|      | GGCGACCGAG | GCTCGTCGTT  | TTCGTGGTGC | CCGCCGTGCC | GACGGGACCC  |
| 1251 | CTGCCTGGTT | AAAGATTATT  | TCCCGGAACC | AGTCACCGTG | AGCTGGAACA  |
|      | GACGGACCAA | TTTCTAATAA  | AGGGCCTTGG | TCAGTGGCAC | TCGACCTTGT  |
| 1301 | GCGGGGCGCT | GACCAGCGGC  | GTGCATACCT | TTCCGGCGGT | GCTGCAAAGC  |
|      | CGCCCCGCGA | CTGGTCGCCG  | CACGTATGGA | AAGGCCGCCA | CGACGTTTCG  |
| 1351 | AGCGGCCTGT | ATAGCCTGAG  | CAGCGTTGTG | ACCGTGCCGA | GCAGCAGCTT  |
|      | TCGCCGGACA | TATCGGACTC  | GTCGCAACAC | TGGCACGGCT | CGTCGTGCGAA |
| 1401 | AGGCACTCAG | ACCTATATTT  | GCAACGTGAA | CCATAAACCG | AGCAACACCA  |
|      | TCCGTGAGTC | TGGATATAAA  | CGTTGCACTT | GGTATTTGGC | TCGTTGTGGT  |
|      |            |             | EcoRI      |            |             |
|      |            |             | ~~~~~      |            |             |
| 1451 | AAGTGGATAA | AAAAGTGGAA  | CCGAAAAGCG | AATTCGGGGG | AGGGAGCGGG  |
|      | TTACCTATT  | TTTTCACCTT  | GGCTTTTCGC | TTAAGCCCCC | TCCCTCGCCC  |
| 1501 | AGCGGTGATT | TTGATTATGA  | AAAGATGGCA | AACGCTAATA | AGGGGGCTAT  |
|      | TCGCCACTAA | AACTAATACT  | TTTCTACCGT | TTGCGATTAT | TCCCCGATA   |
|      |            |             | gIIIseq9   | 100.0%     |             |
|      |            |             | =====      |            |             |
| 1551 | GACCGAAAAT | GCCGATGAAA  | ACGCGCTACA | GTCTGACGCT | AAAGGCAAAC  |
|      | CTGGCTTTTA | CGGCTACTTT  | TGCGCGATGT | CAGACTGCGA | TTTCCGTTTG  |
|      |            |             | ClaI       |            |             |
|      |            |             | ~~~~~      |            |             |
| 1601 | TTGATTCTGT | CGCTACTGAT  | TACGGTGCTG | CTATCGATGG | TTTCATTGGT  |
|      | AACTAAGACA | GCGATGACTA  | ATGCCACGAC | GATAGCTACC | AAAGTAACCA  |
| 1651 | GACGTTTCCG | GCCTTGCTAA  | TGGTAATGGT | GCTACTGGTG | ATTTTGCTGG  |
|      | CTGCAAAGGC | CGGAACGATT  | ACCATTACCA | CGATGACCAC | TAAAACGACC  |
| 1701 | CTCTAATTCC | CAAAATGGCTC | AAGTCGGTGA | CGGTGATAAT | TCACCTTTAA  |
|      | GAGATTAAGG | GTTTACCGAG  | TTCAGCCACT | GCCACTATTA | AGTGGAATTT  |
| 1751 | TGAATAATTT | CCGTCAATAT  | TTACCTTCCC | TCCCTCAATC | GGTTGAATGT  |
|      | ACTTATTAAA | GGCAGTTATA  | AATGGAAGGG | AGGGAGTTAG | CCAACCTTACA |
| 1801 | CGCCCTTTTG | TCTTTGGCGC  | TGGTAAACCA | TATGAATTTT | CTATTGATTG  |
|      | GCGGGAAAAC | AGAAACCGCG  | ACCATTTGGT | ATACTTAAAA | GATAACTAAC  |
| 1851 | TGACAAAATA | AACTTATTCC  | GTGGTGTCTT | TGCGTTTCTT | TTATATGTTG  |
|      | ACTGTTTTAT | TTGAATAAGG  | CACCACAGAA | ACGCAAAGAA | AATATACAAC  |
| 1901 | CCACCTTTAT | GTATGTATTT  | TCTACGTTTG | CTAACATACT | GCGTAATAAG  |
|      | GGTGGAATA  | CATACATAAA  | AGATGCAAAC | GATTGTATGA | CGCATTATTC  |

## HindIII

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1951 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG  
CTCAGAATAA TTCGAAGTGG ACACCTTCACT TTTTACCGCG TCTAACACGC

OGIII3 100.0%

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2001 ACATTTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACCGTT AATATTTTGT  
TGTAACAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAACA

2051 TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG  
ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAA ATTGGTTATC

2101 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG  
CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG  
CAACTACAA CAAGGTCAA CCTTGTTCTC AGGTGATAAT TTCTTGACCC

2201 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA  
TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251 CGAGAACCAT CACCCTAATC AAGTTTTTTTG GGGTCGAGGT GCCGTAAAGC  
GCTCTTGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCC

2301 ACTAAATCGG AACCCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA  
TGATTTAGCC TTGGGATTTT CCTCGGGGGC TAAATCTCGA ACTGCCCTT

2351 AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC  
TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCC

2401 GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC  
CGATCCCGCG ACCGTTTACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451 CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA  
GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT AACTCGTTT

2501 AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT  
TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

2551 TCCATAGGCT CCGCCCCCTT GACGAGCATC AAAAAATCG ACGCTCAAGT  
AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2601 CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC  
GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651 TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT  
ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701 ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA  
TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751 CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG  
GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

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F050164-11501

2801 TGTGCACGAA CCCCCGTTT AGTCCGACCG CTGCGCCTTA TCCGGTAACT  
ACACGTGCTT GGGGGGCAAG TCAGGCTGGC GACGCGGAAT AGGCCATTGA

2851 ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA  
TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCTG

2901 GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA  
CGGTGACCAT TGTCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT

2951 GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGA ACAGTATTTG  
CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCT TGTCATAAAC

3001 GTATCTGCGC TCTGCTGTAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC  
CATAGACGCG AGACGACATC GGTCAATGGA AGCCTTTTTC TCAACCATCG

3051 TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG  
AGAACTAGGC CGTTTGTGTTG GTGGCGACCA TCGCCACCAA AAAACAAAC

3101 CAAGCAGCAG ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA  
GTTTCGTCGC TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAACT

3151 TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAACTC ACGTTAAGGG  
AGAAAAGATG CCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC

3201 ATTTTGGTCA GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT  
TAAAACCAGT CTAGATCGTG GTCCGCAAT TCCCGTGGTT ATTGACGGAA

3251 AAAAAAATTA CGCCCCGCCG TGCCACTCAT CGCAGTACTG TTGTAATTCA  
TTTTTTTAAT GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAACT

3301 TTAAGCATTC TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG  
AATTCGTAAG ACGGCTGTAC CTTCCGTTAGT GTTTGCCGTA CTACTTGGAC

3351 AATCGCCAGC GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA  
TTAGCGGTG CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT

3401 TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA  
ATCACTTTTG CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT

3451 AAAGTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC  
TTTGACCACT TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG

3501 AATAAACCCCT TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT  
TTATTTGGGA AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA

3551 CTTGCGAATA TATGTGTAGA AACTGCCGGA AATCGTCGTG GTATTCACTC  
GAACGCTTAT ATACACATCT TTGACGGCCT TTAGCAGCAC CATAAGTGAG

+1

3601 CAGAGCGATG AAAACGTTTC AGTTTGCTCA TGGAAAACGG TGTAACAAGG  
GTCTCGCTAC TTTTGCAAAG TCAAACGAGT ACCTTTTGCC ACATTGTTCC

3651 GTGAACACTA TCCCATATCA CCAGCTCACC GTCTTTCATT GCCATACGGA  
CACTTGATGAT AGGGTATAGT GGTGAGTGG CAGAAAGTAA CGGTATGCCT

3701 ACTCCGGGTG AGCATTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA  
TGAGGCCAC TCGTAAGTAG TCCGCCGTT CTTACACTTA TTTCCGGCCT

3751 TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC  
 ATTTTGAACA CGAATAAAAA GAAATGCCAG AAATTTTCC GGCATTATAG

3801 CAGCTGAACG GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT  
 GTCGACTTGC CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA

3851 CAAAATGTTT TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA  
 GTTTTACAAG AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT

3901 GTGATTTTTT TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA  
 CACTAAAAAA AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT

3951 CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG  
 GAGTTTTTTA TCGGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC

4001 AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTG GGCACCCAG  
 TTGGAGTGGG CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC

4051 GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG  
 CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

M13 Reverse primer 100.0%

=====

4101 ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATT  
 TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTAA

POST-46T0001

## Figure 15

MS-GPC-1 :

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARQYGHRGGFD  
HWGQGTTLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFNESVFGGGTKLTVL  
G

MS-GPC-6

VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGS  
GGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGYGRYSPDLW  
GQGTTLVTVSS

VL

DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASS  
RATGVPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQYSNLPFTFGQGTKVEIK  
RT

MS-GPC-8

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARSPRYRGAFD  
YWGQGTTLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMPQAVFGGGTKLTVL  
G

MS-GPC-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARQLHYRGGFD  
LWGQGTTLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLTMGVFGGGTKLTVL  
G



MS-GPC-8-6

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARSPRYRGAFD  
YWGQGTLLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFGGGTKLTVL  
G

MS-GPC-8-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARSPRYRGAFD  
YWGQGTLLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVFGGGTKLTVL  
G

MS-GPC-8-17

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARSPRYRGAFD  
YWGQGTLLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSVYVFGGGTKLTVL  
G

MS-GPC-8-27

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATATYYCARSPRYRGAFD  
YWGQGTLLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHVFGGGTKLTVL  
G

MS-GPC-8-6-13

VH

FOOTEST-434-11501

QVQLKESGPALVRPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNM DPVDTATYYCARS PRYRGAFD  
YWGQGT LVT VSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGANYVTWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFGGGTKLTVL  
G

MS-GPC-8-10-57

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID  
WDDDKYYSTSLKTRLTISKDTSKNQVVLMTNM DPVDTATYYCARS PRYRGAFD  
YWGQGT LVT VSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIYDNNQ  
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVFGGGTKLTVL  
G

MS-GPC-8-27-41

VH

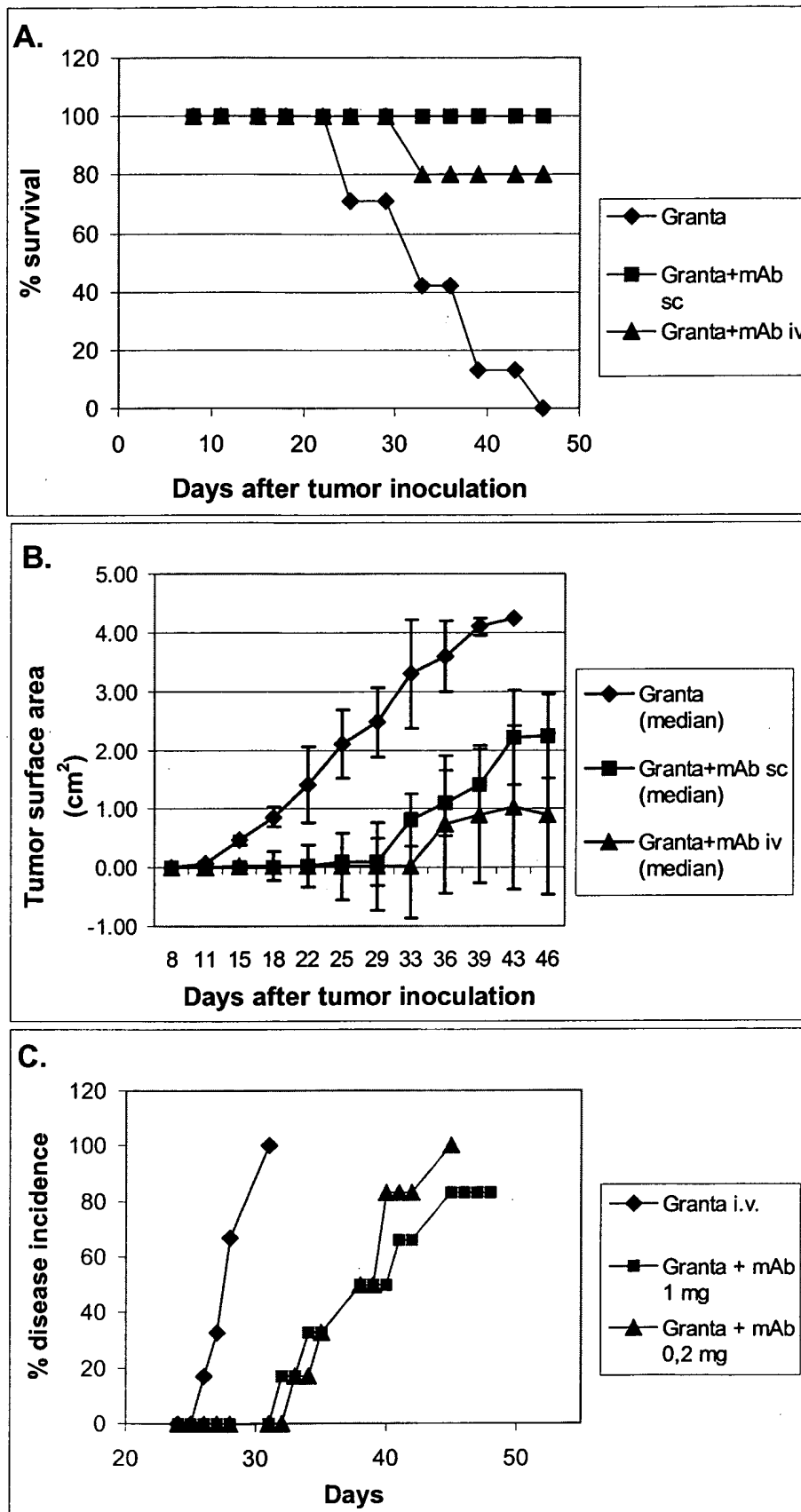
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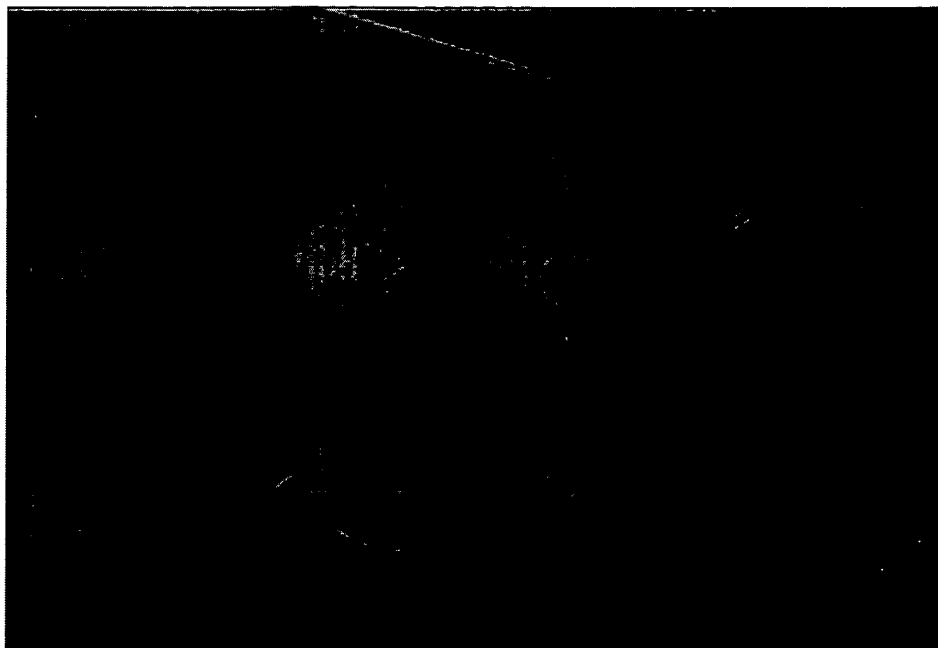
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# Figure 16



## Figure 16 (Cont.)

D



Mouse #2, untreated, day 32; tumor area 4.76 cm<sup>2</sup>

E



Mouse #13, mAb i.v., day 32; tumor area 0.01 cm<sup>2</sup>

FOSTT-HEFTOOL